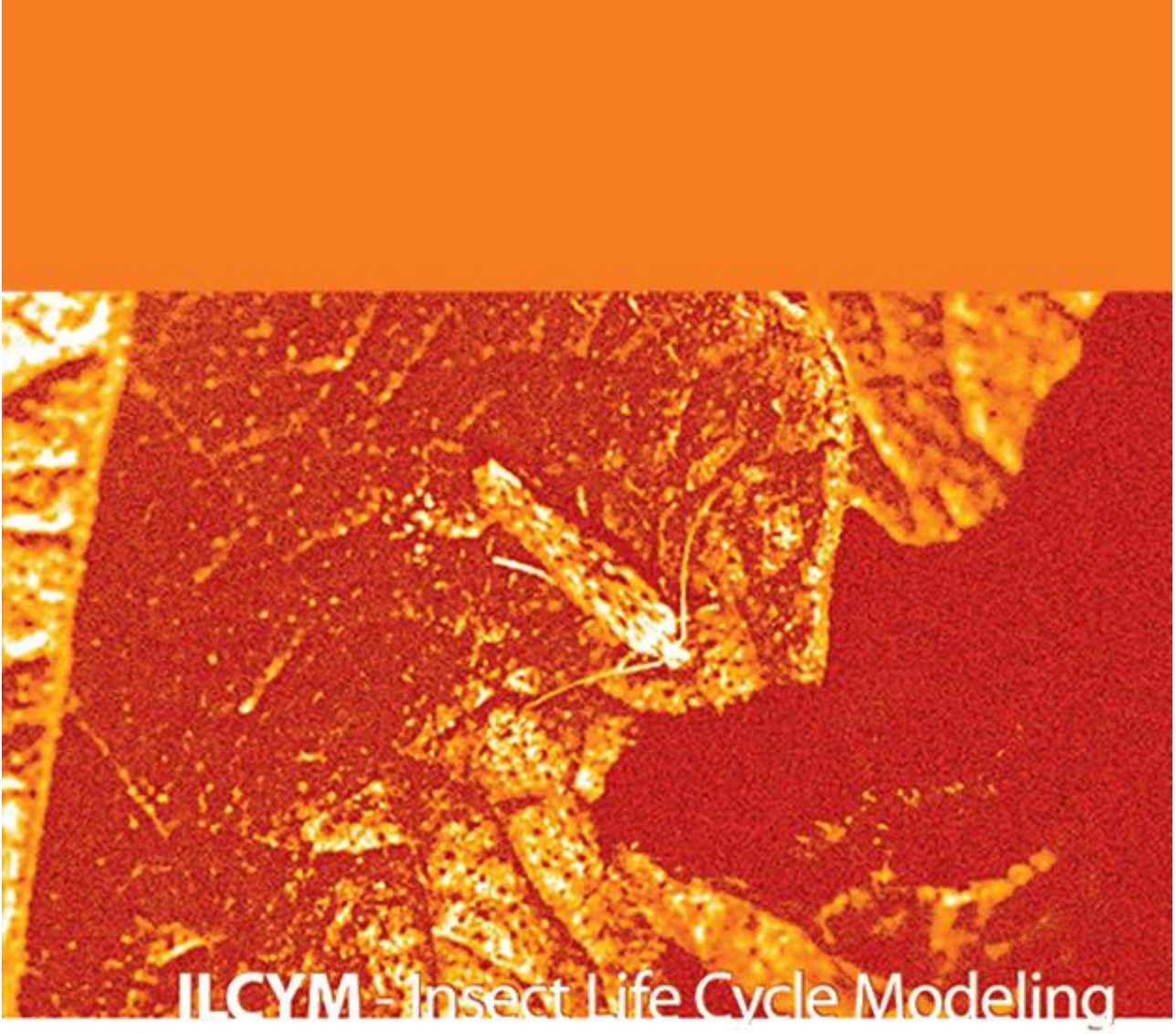

ILCYM - Insect Life Cycle Modeling

A software package for developing temperature-based insect phenology models with applications to regional and global analysis of insect population and mapping

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Insect Life Cycle Modeling (ILCYM, Version 3.0): A software package for developing temperature-based insect phenology models with applications for local, regional and global analysis of insect population and mapping

ILCYM Version 3.0

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Preface

The International Potato Center (CIP) seeks to reduce poverty and achieve food security on a sustained basis in developing countries through scientific research and related activities on potato (*Solanum tuberosum* L.), sweetpotato (*Ipomoea batatas* L. Poir.) and other root and tuber crops, and on the improved management of natural resources in the Andes and other mountain areas. The origin of the potato is the High Andes in South America. Its global distribution began about three hundred years ago, first to Europe and then to other parts of the world. Many potato pests have evolved in the center of origin of the potato. Andean potato weevils of the genus *Premnotrypes* (Coleoptera: Curculionidae) are major problems for potato growers in the Andean region from Venezuela to Bolivia but have fortunately not spread to other potato growing regions outside the Andes. Instead, the potato tuber moth (*Phthorimaea operculella* (Zeller) (Lepidoptera: Gelechidae)) or the leafminer fly (*Liriomyza huidobrensis* (Blanchard) (Diptera: Agromyzidae)) have become invasive in many tropical, subtropical or temperate regions. The potato tuber moth is today reported in more than 90 countries and is considered the most damaging potato pest in the developing world. The leafminer fly, which is highly polyphagous, is reported in 66 countries.

In its global pest management research effort CIPs' Agroecology/IPM team is interested in better understanding pest biology and ecology in order to find out why some species are more invasive than others. We also aim to predict the potential pest population development in different agroecological zones as well as to determine critical infestation periods for better targeting pests during the cropping season. Phenology models for potato pests based on temperature have become important analytical tools in CIP's research program for predicting, evaluating and understanding their population dynamics in agroecosystems under a variety of environmental conditions. At the beginning a temperature-driven phenology model for the potato tuber moth was developed and validated through field and laboratory data which, successfully predicted life-table parameters for different agroecological zones. It was then used to predict the establishment risk and potential pest activity in specific agroecologies according to temperature records. It has also been used to estimate the population structure under given temperatures and allows for performance simulations of field applications and to determine field application rates and frequencies. Further possible applications of these models are manifold.

The approach used to develop and implement the potato tuber moth model can be principally used for other insect species. The strong collaboration between CIPs'

Agroecology/IPM team and the Research Informatics Unit made it possible to develop the software program Insect Life Cycle Modeling (ILCYM version 3.0) with the objective of facilitating the development of further insect phenology models and to provide analytical tools for studying insects' population ecology. It is hoped that the ILCYM software will benefit researchers from national and international agricultural research institutes and universities who either intend to start with insect modeling or want to apply advanced modeling techniques without having the requisite mathematical knowledge or being experts in the field. Ultimately, the application of ILCYM software and modeling results should provide a better understanding of insect's biology and ecology and in the long-term should support a rational decision making process in pest management and improving farmers' food security and daily lives.

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Acknowledgment

The Insect Life Cycle Modeling software described here has been jointly developed by staff members of the Integrated Crop Management Division (ICM Division) and the Research Informatics Unit (RIU) of the International Potato Center (CIP).

We are grateful for the financial support received by the German Federal Ministry for Economic Cooperation and Development (BMZ), Germany and the Regional Fund for Agricultural Technology (FONTAGRO), Washington D.C., without which this software could have not been developed.

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I. INTRODUCTION

Interest in models to predict the environmental suitability for invasive insect pest species has grown radically in the last two decades. In particular, the need to understand the impact of climate change on the potential distribution of pests has accelerated the demand for tools to estimate the potential risk of their invading new environments and agricultural regions. For this purpose, maps are becoming important means of communication using different spatial scales, from local, regional to worldwide to visualize the potential risk of pest distribution and the economic damage it may inflict on crops. Thus, maps are used to inform policy and management in this field to aid in strategic pest management decisions, such as restrictions on the importation of certain crops in international trade, implementation of quarantine measures, the design of pest surveys, etc. (Baker, 1996; Baker *et al.*, 2000; Braasch *et al.*, 1996; McKenney *et al.*, 2003).

Two distinct approaches prevalent in the modelling of insect pests and the risk of establishment and expansion; these can be described as a) “inductive” and b) “deductive”. The “inductive” approach combines through statistical or machine learning methods the known occurrence records of insect species with digital layers of environmental variables. It uses minimal data sets and simple functions to describe the species’ response to temperature and other climatic factors. Generally, presence/absence data or occurrence data only from different locations are sufficient for creating risk maps. The combination of occurrence records and environmental variables can be performed through the application of climate match functions that seek out the establishment potential of an invasive species to new areas by comparing the long-term meteorological data for each selected location where the species is absent with the same data for the location of origin or locations where the species prevails (Sutherst *et al.*, 2000; Sutherst and Maywald, 1991). For applying this approach, computer-aided tools such as CLIMEX (Peacock and Worner, 2006; Vanhanen *et al.*, 2008a; Vanhanen *et al.*, 2008b; Wilmot Senaratne *et al.*, 2006) and BIOCLIM (Kohlmann *et al.*, 1988; Steinbauer *et al.*, 2002) have been developed and used

to predict insect species' demography for pest risk analysis (Rafoss, 2003; Sutherst, 1991; Zalucki and Furlong, 2005) and possible climate change effects (Sutherst and Maywald, 1990).

The "inductive" modelling approach has made considerable advances and a great number of computer programs, including BioMOD, GARP, HABITAT, etc., have been developed (reviewed by Venette *et al.*, 2010). This modelling approach showed advantages where detailed information about insect species is not available; however, critical limitations are the failure to consider the species' biological characteristics in the modelling framework (Venette *et al.*, 2010). Hence, resulting risk maps may inform about potential establishment but they do not provide information on the species population growth and damage potential or temporal population change within a cropping season or year in a given region.

By contrast, the "deductive" approach uses a process-based climatic response model (i.e., phenology model) for a particular insect species of interest. Phenology models are analytical tools for the evaluation, understanding and prediction of the dynamics of insect populations in ecosystems under a variety of environmental conditions and management practices, and more recently they are also being used in phytosanitary risk assessments (Baker, 1991; Jarvis and Baker, 2001a,b). The development of insects, as in other ectothermic organisms, depends on the ambient temperature. This temperature dependency can be applied in a process-oriented framework; forecasting the potential distribution of insect species is completely independent of observed occurrences, and this approach is therefore referred to as "deductive".

The difference between the "inductive" and "deductive" modelling approach is the level of abstraction, which is higher in the "inductive" or "climate match" approach in which the mathematical methods employed lead to a greater generality. Instead, process-based phenology models are either detailed or simplified mathematical models, which describe the basic physiological principles of the insect species' growth, namely its development, survival and reproduction; the complexity of these models can range from simple models with no age structure and limited environmental inputs to age-stage structured

or multi-species models with complex environmental drivers. The two approaches do not necessarily compete, but may also be used to complement each other.

Degree-day models are often used to describe the linear development of insects using the accumulation of temperature above the minimum temperature threshold (Allen, 1976); see Nietschke *et al.* (2007). However, due to the non-linearity of the development curve, especially when temperature deviates from the intrinsic optimal temperature of a species, degree-day models are poor predictors of insect development. This method works well for intermediate temperatures, but produces errors, i.e. significant deviations from the real development, when daily temperature fluctuates to extremes (Stinner *et al.*, 1974; Worner, 1992). Modern, more progressive models use non-linear functions of higher biological significance (i.e. Logan *et al.*, 1976; Sharpe and DeMichele, 1977, etc.), and include stochastic functions for variability in development times among individuals within a population (Sharpe *et al.*, 1981; Wagner *et al.*, 1984).

Computer-aided modelling packages such as DYMEX (Kriticos *et al.*, 2003), NAPPFAST (Nietschke *et al.*, 2008), ECAMON (Trnka *et al.*, 2007) or ILCYM (Sporleder *et al.*, 2007; Sporleder *et al.*, 2009) support the development of process-oriented temperature-driven and age-stage structured insect phenology/population models. The latter, ILCYM (Insect Life Cycle Modeling software, version 3.0), has recently been developed by the International Potato Center (CIP), Lima, Peru and is freely available at http://www.cipotato.org/ilcym/.

This book describes the application of ILCYM software, which supports the development of process-oriented temperature-driven and age-stage structured insect phenology/population models. ILCYM interactively leads the user through the steps for developing insect phenology models, for conducting simulations, and for producing potential population distribution and risk mapping under current or future temperature (climate change) scenarios. The objective of the

present document is to explain how the developed modeling approach works; what type of data need to be generated to develop an insect phenology model (IPhM), what type of data need to be generated to validate a IPhM, how IPhMs are implemented, and what type of insect population analysis will be provided. With the current version of ILCYM the authors intend to share the knowledge gained in insect pest population modeling research at the Agroecology/IPM unit at CIP and provide an open-source computer aided tool, especially for researcher in developing countries, that facilitates the development of own IPhMs using advanced modeling techniques without being experts in the field.

1.1 The modeling approach applied in ILCYM

Modeling of insect populations is for some reasons more complicate than modeling populations of other organisms. Insects pass through different stage before reaching maturity, within these immature stages they may die, and when mature they reproduce. Some species have seasonality (i.e. different life-stages of the insects are only found during specific seasons of the year), others not (i.e. populations are heterogeneous in their age-stage structure because of continuous reproduction and overlapping generations), but their development is always strongly temperature driven. The approach used in ILCYM is to define sub-models describing development and mortality in each immature life-stage of the insect with its variation between individuals in a population, and senescence time and reproduction frequencies of adults according to temperature. These sub-models are based on experimental data obtained through temperature experiments. The reproduction model might include functions for different processes depending on the insect specie under study, i.e. changing sex ratio in adults due to temperature, age-dependent reproduction frequencies, temperature-dependent reproduction frequencies, etc. The overall approach is factor-process based, while temperature is the principle driver (factor) of these processes.

Insects species that show seasonality generally have an over-wintering stage in which the insect hibernates or diapauses. The factors which are responsible to reactivate hibernating insects is often not temperature alone (temperature might

be an indirect factor but for modeling considering temperature alone might not explain this process in its totality). ILCYM's approach is more adequate for insect species that do not hibernate and hence do not show seasonality in its development. However, many components of ILCYM might be used for such species as well.

ILCYM's compiles the established function into a general (generic) phenology model that uses rate summation and a cohort up-dating approach for simulating populations. The cohort up-dating algorithm is based on scheme proposed by Curry *et al.* (1978a) that was further described by Wagner *et al.* (1985) and Logan (1988). In published articles there is not so much discussion on including temperature-induced mortality in immature life stages and recruitment. Both are necessary for more realistic simulation and both are included in ILCYM. Development, reproduction, and survival in insect species describe primarily insect demography; for understanding population dynamics additional knowledge about dispersal and migration, as well as the influence of other biotic or abiotic factors affecting the insects' survival are necessary. The cohort up-dating algorithm calculates population number; it also provides information about the quantitative biology of the insect species under study. Let note that the resulting population increase only represents the potential population growth of the species at a given temperature regime. Real population increase depends on the additional biotic and abiotic factors affecting populations in a given environment. Including such factors would introduce much more complexity into the algorithm, which is not provided in this version of ILCYM. However, when a model for a given species is developed it can directly be applied in ILCYM-GIS environment for spatial analysis; based on real or simulated daily temperature data ILCYM's simulates the potential population increase over time and pest distribution as well as host plan/land covers data for analyzing climate change impact etc.

The steps of developing a model with ILCYM are principally four:

1) Collect the data through conducting temperature experiments or, if available, from the literature.

2) Define the functions describing the temperature-driven processes in insect development using the “model builder” and compile the over-all model (the latter step is done by ILCYM interactively)
3) Validate the model using additional data that were not included for developing the model (generally this data are from experiments conducted under fluctuating temperatures) and conduct sensitivity analysis.
4) Use the model (p.e. for “spatial analysis and mapping” in the third module of ILCYM)

Before and during the development of IPhM, be aware of the following steps:

1) What is the species you are interested in (think first: is the ILCYM approach the right one? How you want to use the model? Modeling is not the purpose itself, there should be another aim why you want to have a model (the purpose might be to learn about the insect biology alone. In any case, researchers who start with the experiments described here will learn something about the species population biology. The knowledge gained can be applied latter for many different purposes).
2) Collect literature on the species for which you want to make a model; what has been done so far? Are literature data available that you can be used for modeling or model validation?
3) Define hypothesis! Finally you are working on a piece of science, and science requires hypothesis.
4) Design and plan your experiment: what do you need (insect rearing facilities, incubators, thermometers or loggers, what are the temperatures you want to test, plan for precision, etc.)? Use dummy data: you may use the dummy data provided in ILCYM to get familiar with the analysis and learn about the approach. You might also create own dummy data with different numbers of temperatures and with different numbers of insects in the experiment for learning about the statistical precision of your planed experiment. Decide about the type of data you want to collect (see chapter on data collection: life-table data

versus cohort studies or mixed – advantages and disadvantages, for your purposes you should know before designing the experiment).

5) Collect the data.
6) Use the “model builder” of ILCYM defining all sub-models for the overall phenology model: at this stage you might start writing a report on results obtained. (What to report?)
7) Once all sub-models are selected, they are compiled to obtain the overall phonology model (ILCYM compiles the overall model automatically according to your initial (interactive) statements writing when starting a new project). It recommended that user’s have some level of familiarity with the structure of the overall phenology model and the modeling approach of ILCYM before starting serious analysis with the software.
8) Conduct sensitivity analysis and validate the model through comparing simulation results with the data from fluctuating temperature experiments or data published in the literature (ILCYM provides tools for that). At this stage you might finalize the report about your model developed.
9) Employ the model for your purposes. You might apply the new model for “pest risk mapping”, which is the third module of ILCYM (i.e. produce maps indicating spatially the potential population growth of a particular pest within a region of interest.

Bear in mind that the data collection might take a long time. At cold temperatures development times of test individuals might be quite long; the whole lifecycle might last more than one year. In such conditions the cohort approach for collecting the data might be better than establishing a life table where a whole life-cycle of one generation need to be monitored. As a role, developing an IPhM should not take longer than one year.

1.2 The conceptual basis of ILCYM

Phenology models predict time of events in an organism's development. Development of many organisms that cannot internally regulate their own

temperature (poikilothermic organisms, ectothermic organisms) is dependent on temperatures to which they are exposed in the environment. Plants and invertebrates, including insects and nematodes, require a certain amount of heat to develop from one point in their life-cycle to another, e.g., from eggs to larvae. Because of yearly variations in weather, calendar dates are not a good basis for making management decisions. Measuring the amount of heat accumulated over time provides a physiological time scale that is biologically more accurate than calendar days.

Phenology models for insect species based on temperature are important analytical tools for predicting, evaluating, and understanding the dynamics of populations in ecosystems under a variety of environmental conditions. The International Potato center (CIP) initially developed a temperature-driven phenology model for the potato tuber moth, *Phthorimaea operculella* Zeller (Lepidoptera: Gelechidae), which well predicted the life-table parameters in different agro-ecological zones. This model was validated through field and laboratory data. It was used to predict the establishment risk and potential pest activity in specific agro-ecologies according to temperature records. Linked with geographic information systems (GIS) and atmospheric temperature the model allowed simulation of three risk indices on a worldwide scale and was also used to predict potential future changes in these indices that may be caused by global warming.

The success of the approach used on developing and implementing the *P. operculella* model stimulated the extension to other insect species. CIP therefore, developed the Insect Life Cycle Software (ILCYM) version 3.0 presented in this manual. The main goal of the software is to facilitate the development of insect phenology models and provide analytical tools for studying insect population ecology.

The authors are aware that a single modeling approach does not fit to every insect species of interest and that it cannot meet every purpose for which a model needs to be developed. However, it is believe that the approach presented here might be a model applicable to many insect species and in

many circumstances for which insect phenology models are developed. An important issue in integrated pest management (IPM) research is to evaluate the potential effects of certain pest management strategies. Parasitoid life tables can be analyzed in the ILCYM “Model builder” and parasitoid phenology models obtained, then applied in ILCYM-GIS component to identify regions in which the parasitoid can potentially establish and control its host (an insect pest). This is an important analysis for planning classical biological control and identifying potential parasitoid release sites. For the development of a two-species interaction model, a parasitism rate function is used for linking the parasitoid and the host (pest) phenology models through a deterministic simulation procedure under constant and varying temperature conditions. This process uses the predicted temperature-dependent development times and parasitoid fertility rates for simulations of the host population growth and development.

1.3 Data

ILCYM analyzes data of different types. The question in modeling the effects of temperature on insect population development is not so much a question of “what data should be collected”, but rather “how these data should be used”. Therefore, ILCYM allows the use of different types of experimental data as input information for developing a pest phenology model; however, the data should allow modeling of the species whole life cycle and should be arranged in a manner to meet certain criteria employed within the software. Data collection and its arrangement to be used as input data in ILCYM is the topic of this section.

1.4 Life table data

Studying insect population ecology is often based on life table studies. A life table is conducted by following a population of n = x individuals from its birth up to the birth of all progeny of these individuals. Events like death or reproduction are monitored in equal time interval (hours, days, years, etc., depending on the organism under study). This methodology is used for populations of many organisms, including humans and other animal populations, to describe the life

expectancy of individuals (life insurance companies use this to estimate the probability of death of a person of certain age) and their reproduction capacity. Specific statistics were developed to calculated “life table parameters”, describing the population growth according to the Malthusian law of population increase. Life table analysis is broadly employed in studying populations; however, since the life cycle is more complicate in insects (due to different immature life stages) than in other animals several modifications were made in ILCYM software.

For constructing a life-table for an insect cohort (i.e. a group of individual of the same age), the experiment generally starts from "eggs" that were all laid within the same time period; p.e. within the last 12 or 24 hours. The number of eggs used should be at least $n \geq 100$ because during each life stage holds certain proportion of the insects that might die and the number of individuals entering each subsequent life stage will be hence reduced. Then the number of individuals observed might be insufficient for the last life stages or the number of females might be insufficient to assess well fecundity. It would be recommendable to have at least 30 surviving females in the experiment for assessment of fecundity. Especially, the number of insects used for constructing a life table at extreme high and low temperatures, where mortality is generally high, should be increased because of the expected increased mortality during immature life stages. The number of individual used for life tables at different temperatures need not to be balanced. Analysis of these data will include weights that account for differences in numbers of individuals that entered a certain life stage at a given temperature. Life tables can be repeated at the same temperatures with another batch of individuals (cohort) from the population. Also the number of life tables in each temperature does not need to be balanced. In the analysis data from the same temperature (replications) can be pooled or used separately when fitting models for describing temperature effects on insect development or fecundity; however, if the temperature for repeated life tables deviated by more than 1ºC the data should not be pooled but submitted separately to the analysis.

1.4.1 Data records for “complete life tables”

Data for each life table can be arranged in an ordinary spreadsheet. The life stage of each individual of the cohort is traced in one column (i.e. number of columns = *n*). The state of each individual is noted in rows for each evaluation time (generally one day) until the last individual of the cohort has died. An example is given in Figure 1. For each individual surviving the development stage, which is in the example given “egg”, “larva”, or “pupa”, is recorded for each evaluation time (indicated in the spreadsheet as “E” = egg, ”L” = larva, and “P” = pupa). The evaluation interval is generally one day; however, the evaluation time might be changed; for example 12 h, 8 h, etc.; however, the interval should be constant throughout the experiment and always the same in all life tables constructed at different constant temperatures that enter the analysis for developing the phenology model in ILCYM. The number of life stages to be evaluated depends on the species under study and needs to be chosen by the investigator. Letters for indicating each life stage can be freely chosen. Non-survivors are marked always as "dead". Emergence of male adults will be recorded as "M" while for living female adults the number of eggs laid per female during the evaluation interval is noted.

Excurse: Notes on the evaluation interval: Since at high temperatures the development is faster than at low temperatures it could be that the interval of one day might be too broad for determining well the variation in insect development to the next stage. In the example given (Figure 1) all eggs remained egg at the 4^{th} evaluation and had developed into larvae at the 5^{th} evaluation. Therefore, these data would not provide good information to assess the distribution curve for the development from eggs into larva. The median development time would be expected to be between 4 and 5 days but its real value and the slope of the distribution curve cannot be assessed. In this case it would be helpful to reduce the interval time to 8 or 12 hours for obtaining at least one data point in which the proportion of subjects developed into larvae is higher than 0% and lower than 100%. For lower temperatures, such a shallow evaluation interval probably would be not necessary because the development time increases significantly and the development time distribution curve could

be well established even when a broader evaluation interval would have been used; for example of 2 days. The evaluation interval could be differently chosen specifically to each temperature evaluated; however, in the data spreadsheets used for developing IPhM in ILCYM the interval (rows) needs to be the same in all life tables (temperatures). Therefore, even if the interval used for one life table was for example 2 days and the interval used for the life table at the highest temperature was 12 hours all spreadsheets need to be filled using an 8 hour interval.

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	E	E	E	E	E	E	E	E	E	E	E	…. ….	E
2	E	E	E	E	E	E	E	E	E	E	E	…. ….	E
3	E	E	E	E	E	E	E	E	E	E	E	…. ….	E
4	E	E	E	E	E	E	E	E	E	E	E	…. ….	E
5	L	L	L	L	L	L	L	L	L	L	L	…. ….	L
6	L	L	L	L	L	L	L	L	L	L	L	…. ….	L
7	L	L	L	L	L	L	L	L	L	L	L	…. ….	L
8	L	L	L	L	L	L	L	L	L	L	L	…. ….	L
9	L	L	L	L	L	L	L	L	L	L	L	…. ….	L
10	L	L	L	L	L	L	L	L	L	L	L	…. ….	L
11	L	L	L	L	L	L	L	L	L	L	L	…. ….	L
12	L	L	L	L	L	L	L	L	L	L	L	…. ….	L
13	L	L	L	L	L	L	L	L	L	L	L	…. ….	L
14	P	P	dead	P	P	P	P	L	L	L	L	…. ….	L
15	P	P	dead	P	P	P	P	P	P	P	P	…. ….	P
16	P	P	dead	P	P	P	P	P	P	P	P	…. ….	P
17	P	P	dead	P	P	P	P	P	P	P	P	…. ….	P
18	P	P	dead	P	P	P	P	P	P	P	P	…. ….	P
19	P	M	dead	P	P	P	P	P	P	P	P	…. ….	P
20	M	M	dead	18	13	M	14	P	P	P	P	…. ….	dead
21	M	M	dead	25	17	M	18	4	5	M	M	…. ….	dead
22	M	M	dead	21	13	M	17	22	20	M	M	…. ….	dead
23	M	M	dead	11	4	M	4	13	20	M	M	…. ….	dead
24	M	M	dead	6	6	M	6	10	12	M	M	…. ….	dead
25	M	M	dead	3	2	M	3	6	6	M	M	…. ….	dead
26	M	M	dead	2	1	M	2	4	4	M	M	…. ….	dead
27	M	M	dead	1	2	M	1	1	1	M	M	…. ….	dead
28	M	M	dead	1	1	M	1	1	1	M	M	…. ….	dead
29	M	M	dead	dead	dead	M	dead	0	1	M	M	…. ….	dead
30	M	dead	dead	dead	dead	dead	dead	dead	0	M	M	…. ….	dead
31	dead	dead	dead	dead	dead	dead	dead	dead	dead	M	M	…. ….	dead
32	dead	dead	dead	dead	dead	dead	dead	dead	dead	dead	dead	…. ….	dead

Figure 1: Example for recording life table data in a spreadsheet. Each column represents an individual and its state (life stage) is recorded in a constant time interval (generally one day) until its death. Different development stages of the species are recorded by using stage-specific letters. Adult males are marked as “M” and for surviving females the number of eggs laid per evaluation interval is recorded. For further explanations see the text.

For subjects that remained in the same stage as in the 2-day earlier evaluation the state of subject is clear for the missing time intervals and can be filled; however, if a subject developed within this 2-day interval into the next stage then the state is unclear for the missing intervals. In that case missing values need to be filled. ILCYM will handle these data as “interval censored data” (i.e.

development between interval “x” and interval “x-2 days”. For further information on this merit see section “data analysis”.

Transforming spreadsheet data into the format for analysis in ILCYM

ILCYM software only run data in text formats. Data organized in a spreadsheet need to transform in test format with the extension .txt (see. Figure). For easy identification of the data it is recommended to include the following identifiers in the document’s name: Species name, evaluated temperature (and optionally a number that indicates the replication at a given temperature), and the interval; p.e. “Phthorimaea-operculella_28-1_1d”; that is, *Phthorimaea operculella* was the species used in this experiment, incubation temperature was constantly 28ºC and it was the first life table constructed at this temperature, and the evaluation interval between rows in the document is one day.

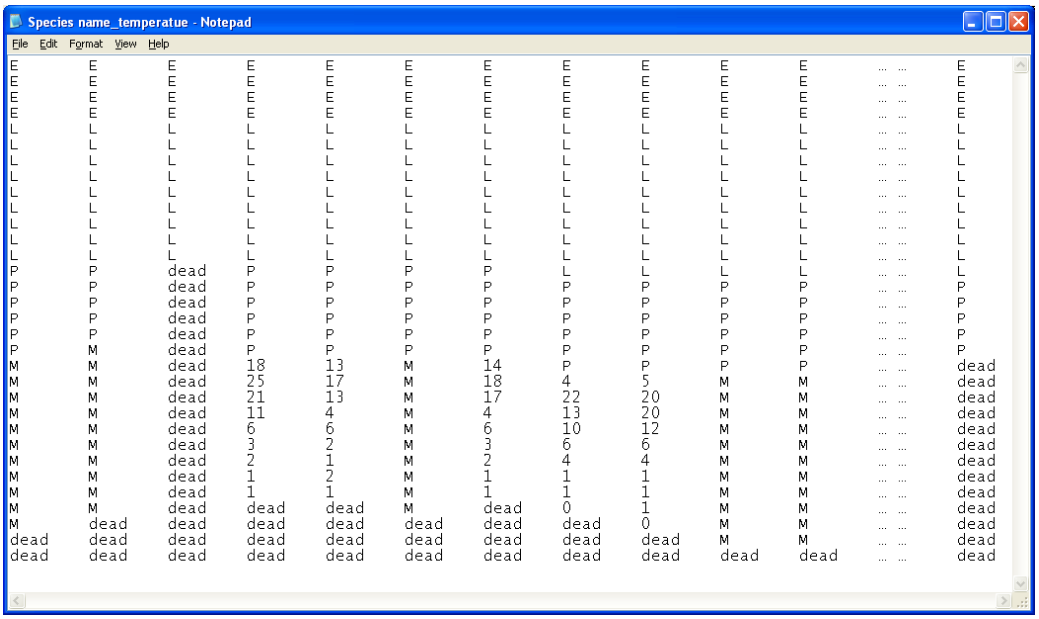

Species name_temperatue - Notepad
File Edit Format View Help
E E E E E E E E E E E ... ... E
E E E E E E E E E E E ... ... E
E E E E E E E E E E E ... ... E
E E E E E E E E E E E ... ... E
L L L L L L L L L L L L
L L L L L L L L L L L L
L L L L L L L L L L L L
L L L L L L L L L L L L
L L L L L L L L L L L L
L L L L L L L L L L L L
L L L L L L L L L L L L
L L L L L L L L L L L L
L L L L L L L L L L L L
P P dead P P P P L L L L L
P P dead P P P P P P P P ... ... P
P P dead P P P P P P P P ... ... P
P P dead P P P P P P P P ... ... P
P P dead P P P P P P P P ... ... P
P M dead P P P P P P P P ... ... P
M M dead 18 13 M 14 P P P P ... ... dead
M M dead 25 17 M 18 4 5 M M ... ... dead
M M dead 21 13 M 17 22 20 M M ... ... dead
M M dead 11 4 M 4 13 20 M M ... ... dead
M M dead 6 6 M 6 10 12 M M ... ... dead
M M dead 3 2 M 3 6 6 M M ... ... dead
M M dead 2 1 M 2 4 4 M M ... ... dead
M M dead 1 2 M 1 1 1 M M ... ... dead
M M dead 1 1 M 1 1 1 M M ... ... dead
M M dead dead dead M dead 0 1 M M ... ... dead
M dead dead dead dead dead dead dead 0 M M ... ... dead
dead dead dead dead dead dead dead dead dead M M ... ... dead
dead dead dead dead dead dead dead dead dead dead dead ... ... dead

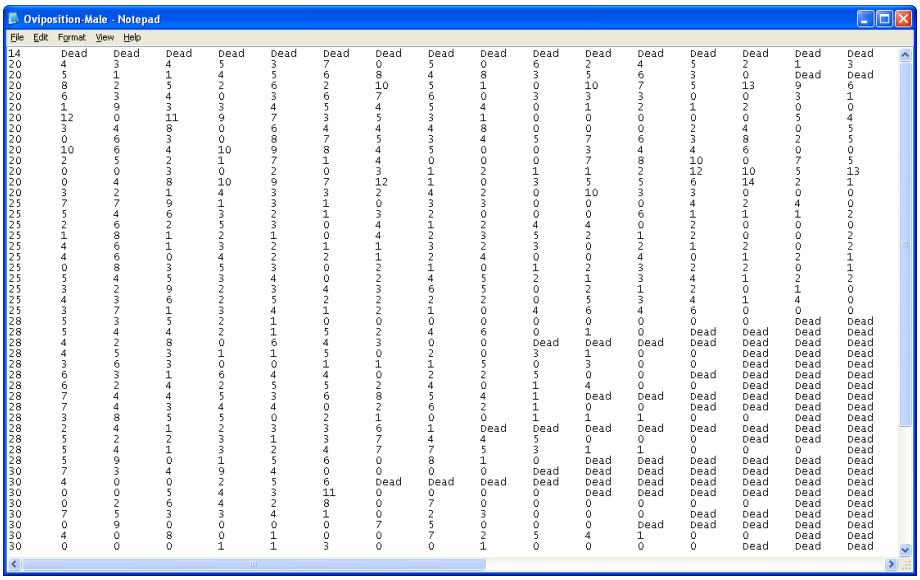
Figure 2: Life table data text file generated by saving the above spreadsheet as txt-file (tab-delimited) for use in ILCYM. The file name should indicate the species name studied and the temperature at which the life table was constructed.

If the female rate in the progeny is expected to be variable:

In case that the female rate in the progeny is not constant but possibly affected by temperature or female age all eggs need to be further reared in batches (the eggs from each individual female during one evaluation interval can be reared

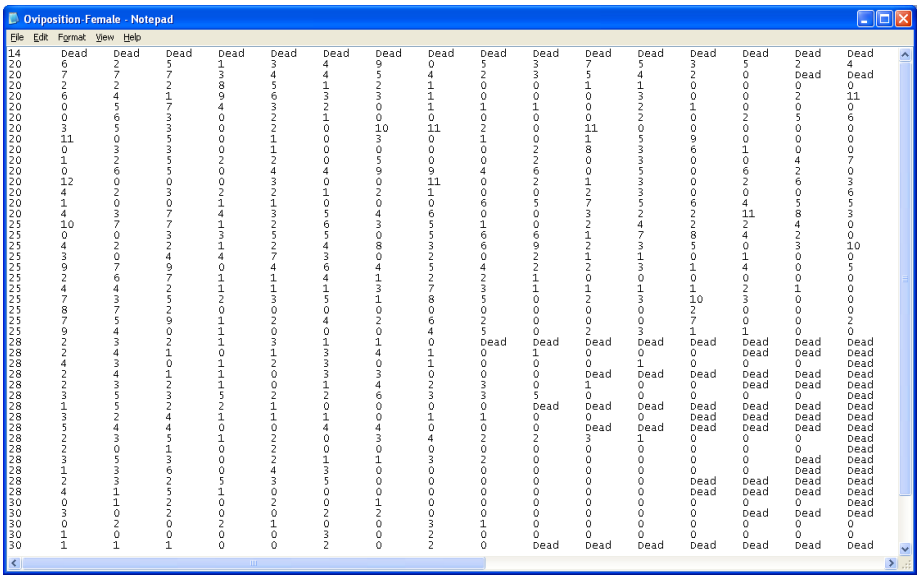
jointly) to adult stage and their sex determined. The data can be arranged as shown in Figure 3 for analysis in ILCYM.

A



14	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead
20	4	3	4	5	3	7	0	5	0	6	2	4	5	2	1	3
20	5	1	1	4	5	6	8	4	8	3	5	6	3	0	Dead	Dead
20	8	2	5	2	6	2	10	5	1	0	10	7	5	13	9	6
20	6	3	4	0	3	6	7	6	0	3	3	3	0	0	3	1
20	1	9	3	3	4	5	4	5	4	0	1	2	1	2	0	0
20	12	0	11	9	7	3	5	3	1	0	0	0	0	0	5	4
20	3	4	8	0	6	4	4	4	8	0	0	0	2	4	0	5
20	0	6	3	0	8	7	5	3	4	5	7	6	3	8	2	5
20	10	6	4	10	9	8	4	5	0	0	3	4	4	6	0	0
20	2	5	2	1	7	1	4	0	0	0	7	8	10	0	7	5
20	0	0	3	0	2	0	3	1	2	1	1	2	12	10	5	13
20	0	4	8	10	9	7	12	1	0	3	5	5	6	14	2	1
20	3	2	1	4	3	3	2	4	2	0	0	10	3	3	0	0
25	7	7	9	1	3	1	0	3	3	0	0	0	4	2	4	0
25	5	4	6	3	2	1	3	2	0	0	0	6	1	1	1	2
25	2	6	2	5	3	0	4	1	2	4	4	0	2	0	0	0
25	1	8	1	2	1	0	4	2	3	5	2	1	2	0	0	2
25	4	6	1	3	2	1	1	3	2	3	0	2	1	2	0	2
25	4	6	0	4	2	2	1	2	4	0	0	4	0	1	2	1
25	0	8	3	5	3	0	2	1	0	1	2	3	2	2	0	1
25	5	4	5	3	4	0	2	4	5	2	1	3	4	1	2	2
25	3	2	9	2	3	4	3	6	5	0	2	1	2	0	1	0
25	4	3	6	2	5	2	2	2	2	0	5	3	4	1	4	0
25	3	7	1	3	4	1	2	1	0	4	6	4	6	0	0	0
28	5	3	5	2	1	0	0	0	0	0	0	0	0	0	Dead	Dead
28	5	4	4	2	1	5	2	4	6	0	1	0	Dead	Dead	Dead	Dead
28	4	2	8	0	6	4	3	0	0	Dead	Dead	Dead	Dead	Dead	Dead	Dead
28	4	5	3	1	1	5	0	2	0	3	1	0	0	Dead	Dead	Dead
28	3	6	3	0	0	1	1	1	5	0	3	0	0	Dead	Dead	Dead
28	6	3	1	6	4	4	0	2	2	5	0	0	Dead	Dead	Dead	Dead
28	6	2	4	2	5	5	2	4	0	1	4	0	0	Dead	Dead	Dead
28	7	4	4	5	3	6	8	5	4	1	Dead	Dead	Dead	Dead	Dead	Dead
28	7	4	3	4	4	0	2	6	2	1	0	0	Dead	Dead	Dead	Dead
28	3	8	5	5	0	2	1	0	0	1	1	1	0	0	Dead	Dead
28	2	4	1	2	3	3	6	1	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead
28	5	2	2	3	1	3	7	4	4	5	0	0	0	Dead	Dead	Dead
28	5	4	1	3	2	4	7	7	5	3	1	1	0	0	0	Dead
28	5	9	0	1	5	6	0	8	1	0	Dead	Dead	Dead	Dead	Dead	Dead
30	7	3	4	9	4	0	0	0	0	Dead	Dead	Dead	Dead	Dead	Dead	Dead
30	4	0	0	0	2	5	6	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead
30	0	0	5	4	3	11	0	0	0	0	Dead	Dead	Dead	Dead	Dead	Dead
30	0	2	6	4	2	8	0	7	0	0	0	0	0	0	Dead	Dead
30	7	5	3	3	4	1	0	2	3	0	0	0	0	Dead	Dead	Dead
30	0	9	0	0	0	1	0	7	5	0	0	0	Dead	Dead	Dead	Dead
30	4	0	8	0	1	0	0	7	2	5	4	1	0	0	Dead	Dead
30	0	0	0	1	1	3	0	0	1	0	0	0	0	Dead	Dead	Dead

B



14	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead
20	6	2	5	1	3	4	9	0	5	3	7	5	3	5	2	4
20	7	7	3	4	4	5	4	2	3	5	4	2	0	Dead	Dead	Dead
20	2	2	2	8	5	1	2	1	0	0	1	1	0	0	0	0
20	6	4	1	9	6	3	3	1	0	0	0	3	0	0	2	11
20	0	5	7	4	3	2	0	1	1	1	0	2	1	0	0	0
20	0	6	3	0	2	1	0	0	0	0	0	2	0	2	5	6
20	3	5	3	0	2	0	10	11	2	0	11	0	0	0	0	0
20	11	0	5	0	1	0	3	0	1	0	1	5	9	0	0	0
20	0	3	3	0	1	0	0	0	0	2	8	3	6	1	0	0
20	1	2	5	2	2	4	0	5	0	0	2	0	3	0	0	4	7
20	0	6	5	0	4	4	9	9	4	6	0	5	0	6	2	0
20	12	0	0	0	3	0	0	11	0	2	1	3	0	2	6	3
20	4	2	3	2	2	1	2	1	0	0	2	3	0	0	0	6
20	1	0	0	1	1	0	0	0	6	5	7	5	6	4	5	5
20	4	3	7	4	3	5	4	6	0	0	3	2	2	11	8	3
25	10	7	7	1	2	6	3	5	1	0	2	4	2	2	4	0
25	0	0	3	3	5	5	0	5	6	6	1	7	8	4	2	0
25	4	2	2	1	2	4	8	3	6	9	2	3	5	0	3	10
25	3	0	4	4	7	3	0	2	0	2	1	1	0	1	0	0
25	9	7	9	0	4	6	4	5	4	2	2	3	1	4	0	5
25	2	6	7	1	1	4	1	2	2	1	0	0	0	0	0	0
25	4	4	2	1	1	1	3	7	3	1	1	1	1	2	1	0
25	7	3	5	2	3	5	1	8	5	0	2	3	10	3	0	0
25	8	7	2	0	0	0	0	0	0	0	0	0	2	0	0	0
25	7	5	9	1	2	4	2	6	2	0	0	0	7	0	0	2
25	9	4	0	1	0	0	0	4	5	0	2	3	1	1	0	0
28	2	3	2	1	3	1	1	0	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead
28	2	4	1	0	1	3	4	1	0	1	0	0	0	Dead	Dead	Dead
28	4	3	0	1	2	3	0	1	0	0	0	1	0	0	0	Dead
28	2	4	1	1	0	3	3	0	0	0	Dead	Dead	Dead	Dead	Dead	Dead
28	2	3	2	1	0	1	4	2	3	0	1	0	0	Dead	Dead	Dead
28	3	5	3	5	2	2	6	3	3	5	0	0	0	0	0	Dead
28	1	5	2	2	1	0	0	0	0	0	Dead	Dead	Dead	Dead	Dead	Dead
28	3	2	4	1	1	1	0	1	1	0	0	0	Dead	Dead	Dead	Dead
28	5	4	4	0	0	4	4	0	0	0	Dead	Dead	Dead	Dead	Dead	Dead
28	2	3	5	1	2	0	3	4	2	2	3	1	0	0	0	Dead
28	2	0	1	0	2	0	0	0	0	0	0	0	0	0	0	Dead
28	3	5	3	0	2	1	1	3	2	0	0	0	0	0	Dead	Dead
28	1	3	6	0	4	3	0	0	0	0	0	0	0	0	Dead	Dead
28	2	3	2	5	3	5	0	0	0	0	0	0	0	Dead	Dead	Dead
28	4	1	5	1	0	0	0	0	0	0	0	0	0	Dead	Dead	Dead
30	0	1	2	0	2	0	1	0	0	0	0	0	0	0	0	Dead
30	3	0	2	0	0	2	2	0	0	0	0	0	0	0	Dead	Dead
30	0	2	0	2	1	0	0	3	1	0	0	0	0	0	0	0
30	1	0	0	0	3	3	0	2	0	0	0	0	0	0	0	0
30	1	1	1	0	0	2	0	2	0	Dead	Dead	Dead	Dead	Dead	Dead	Dead

Figure 3: Example for arranging the data in text file for differentiating between female and male individuals in the progeny; above (A): data for males reproduced, below (B): data for reproduced females. In both data files, the first column represents the temperature and the subsequent columns represent number of egg laid by the individual in a constant time interval (generally one day) until its death.

If only temperature is expected to affect the female rate in the progeny but not female age the eggs obtained from each temperature tested can be reared together (pooled) because then the effect of female age will not be analyzed; in that case the female rate is considered to be constant throughout the life-span of female adult.

1.4.2 Data records for "incomplete life tables"

The life-tables would be incomplete if the cohorts' history were followed-up until insects have reached the adult stage. Data recording would be the same as for "complete" life tables but only the event of male and female emergences would be indicated. After adult emergence the survival time of adults would not be further monitored and hence the columns can indicated as "dead" in the subsequent cells of the row. Data for a single life table would look as shown in Figure 2. Reproduction would be assessed with other subjects in additional experiments at the same temperatures and adult survival time would be retrieved from these experiments.

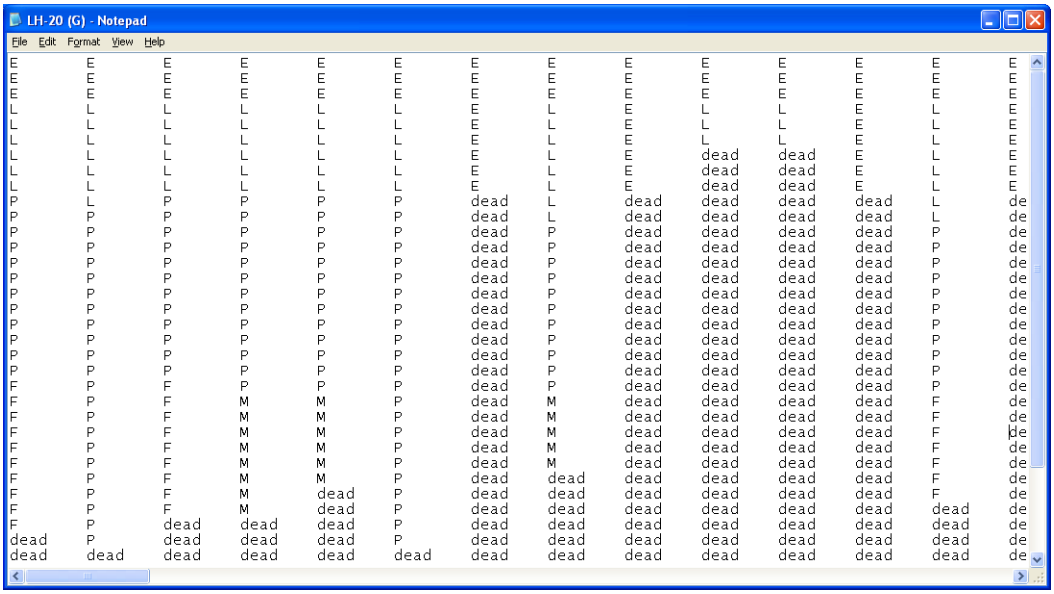


Figure 4 Example for recording "incomplete" life table data at constant temperature (20°C) in a text file. As for "complete" life table each column represents an individual and its state (life stage) is recorded in a constant time interval (generally one day) until its death or development into adult. Survival time of adults is not monitored further because adult survival time will be assessed in an additional experiment for determining adult survival time and oviposition; however, emergence of males ("M") and females ("F") is recorded.

The oviposition-file for each temperature would look as shown in Figure 3; either a single file if the female rate is constant over all temperatures or two files, one for reproduced males and one for reproduced females, if the female rate is expected to be variable.

1.4.3 Cohort studies

In cohort studies, the structure of data for the analysis in ILCYN is different. Survival time and mortality is assessed in the same way as for “life tables” but for a single life stage only. Data are arranged by specific life stages; i.e. there is one data file for each life stage in the life history of the insect under study. For example, if the life history of the species comprises three immature life stages, i.e. egg, larva, and pupa, five files are required, that is one for “Egg”, one for “Larva”, one for “Pupa” stages, and one for “Female adults” and “Male adults” survival each. In addition, one or two oviposition-files are required depending if the female rate in the species is constantly the same across temperatures or if the female rate needs to be evaluated from the data (variable rate). The latter is when temperature affects the “female rate” or if the female rate is expected to change with female adult age. Data on oviposition need to be retrieved from the same cohort of adults (“female adults”) used to establish the overall model. Researcher can freely chose the number of life stages according to their choices or requirement; for example the larva-stage can be separated by specific larval instars (L_1, L_2 L_3, etc.), or a “prepupal” stage could be includes. Important is that the whole life cycle is covered and that there is no overlapping when assessing the development/survival time of individual life stages/instars. There should be a clear definition when each single life stage/instar is completed and the insects used to initiate a cohort study should be of this specific physiological age.

An example for arranging the data is given in Figure 5. The data file contains 4 columns of which the first column represents the temperature used (in the example a total of 7 temperatures were evaluated), second column indicates the evaluation time after experiment set-up (records should start from the evaluation before first development was observed) here measured as “days-

after-experiment set-up"), third column indicates the number of insects used in each temperature, and the forth column indicates the number of individual that had developed to the next stage on each evaluation date. In "life table" studies the evaluation interval needs to be always the same for calculating life table parameters. Such condition is not needed with "cohort study" however, missing evaluations should not be included in file (for example, if the cohort was evaluated after 3 days and again after 5 days, and in day 4 no evaluation was conducted, day 4 should not appear in the records).

A

	A	B	C	D
1	10.6	32	1000	0
2	10.6	33	1000	69
3	10.6	34	1000	165
4	10.6	35	1000	141
5	10.6	36	1000	183
6	10.6	37	1000	145
7	10.6	38	1000	74
8	10.6	39	1000	1
9	10.6	40	1000	0
10	15	14	300	0
11	15	15	300	50
12	15	16	300	91
13	15	17	300	87
14	15	18	300	28
15	15	19	300	4
16	15	20	300	0
17	16.1	9	1000	0
18	16.1	10	1000	61
19	16.1	11	1000	111
20	16.1	12	1000	394
21	16.1	13	1000	216
22	16.1	14	1000	31
23	16.1	15	1000	15
24	16.1	16	1000	0
25	20.3	6	1000	0
26	20.3	7	1000	32
27	20.3	8	1000	699
28	20.3	9	1000	126
29	20.3	10	1000	1
30	20.3	11	1000	0
31	23	5	800	0
32	23	6	800	525
33	23	7	800	162
34	23	8	800	1
35	23	9	800	0
36	24	4	400	0
37	24	5	400	174
38	24	6	400	190
39	24	7	400	0
40	26.1	3	700	0
41	26.1	4	700	92
42	26.1	5	700	513
43	26.1	6	700	11
44	26.1	7	700	0
45	26.7	4	400	0
46	26.7	5	400	323
47	26.7	6	400	13
48	26.7	7	400	2
49	26.7	8	400	0
50	31	2	1400	0
51	31	3	1400	246
52	31	4	1400	992
53	31	5	1400	6
54	31	6	1400	0

B

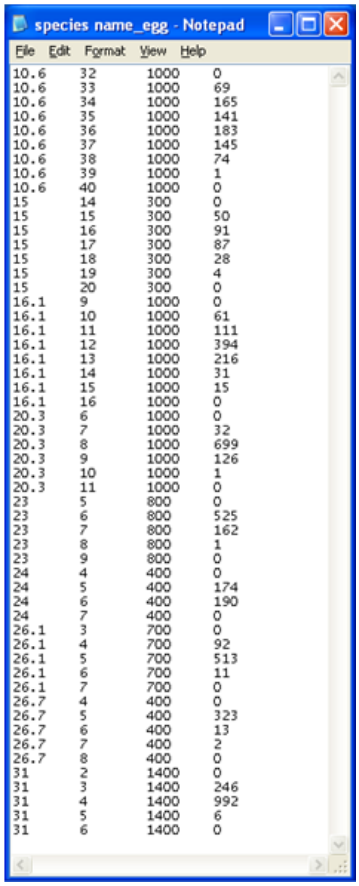


Figure 5: Example for recording "cohort study" data in a spreadsheet (A) and the same data saved as a txt-file (tab-delimited) (B) for use in ILCYM. The first column indicates the temperature evaluated (here a total of 7 temperatures were tested), second column indicates the evaluation intervals number (here measured as "days-after-experiment set-up"), third column indicates the number of insects used in each temperature, and the forth column indicates the number of individual that had developed to the next stage on each evaluation date. For further explication see the text.

ILCYM handle such data as “interval censored data” and retrieves the interval limits from the previous row (i.e. development between day “3” and day “5” after experiment set-up. The recording should be continued until the last individual of the cohort developed to the next stage or died. ILCYM retrieves the mortality rate in each life stage for each temperature from the number of individuals used and the number of individuals that developed to the next stage (survivors). Evaluations that resulted in “zero” observations (change of stage) need to be included in the record; otherwise ILCYM would not determine well the time span in which the individuals developed to the next stage.

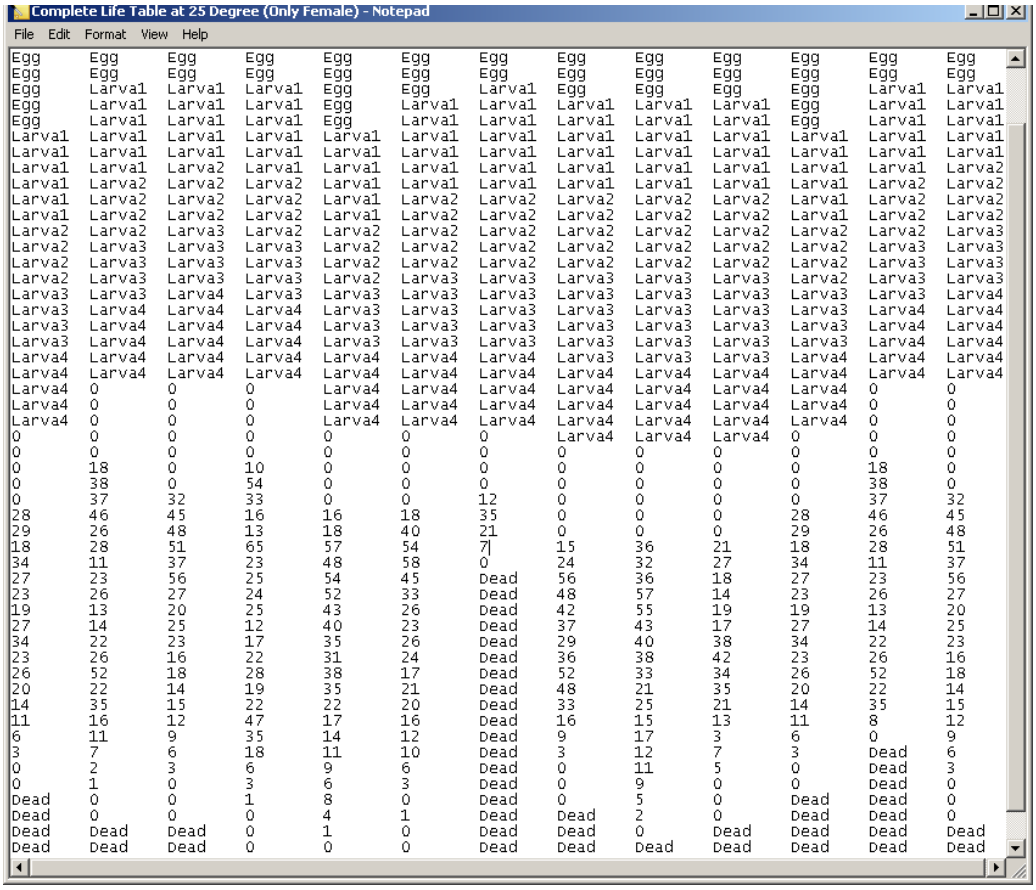
Data for adults (survival time of males and females) are recorded in the same manner. The difference is that adults do not develop into another stage but die. Hence the number of insects tested (column 3) should be equal to the sum of individuals that were recorded as dead over all evaluation for a single temperature. No additional mortality rate is calculated as for the immature life stages. The oviposition data are recorded as described above for “life table” data. The number of eggs oviposited should be retrieved for the cohort of females included in this experiments.

Data type dealing with only female population

ILCYM authors recommend two-sex life table to be used as input data to the software as described above. This is because most insect species (Lepidoptera, Coleoptera, Orthoptera, and Diptera) are bisexual having both males and females, and both sexes may cause economical loss or be vectors of disease. In addition, there is variation in developmental rate among individual and between sexes in natural population. However traditional way of collecting life table Lotka (1907) only deal with female population and ignore the raisons mentioned earlier.

For complete life table data arrangement are similar as explained above where life stage of each individual is traced in one column and the state of each individual is noted in rows for each evaluation time until the last individual of the group has died. The main difference here is the absence of male progeny.

For cohort study, the data arrangement is identical to the description provided above; only that male file is omitted. Below is an example file for complete life table at a given temperature.


Complete Life Table at 25 Degree (Only Female) - Notepad
File Edit Format View Help
Egg Egg Egg Egg Egg Egg Egg Egg Egg Egg Egg Egg Egg
Egg Egg Egg Egg Egg Egg Egg Egg Egg Egg Egg Egg Egg
Egg Larva1 Larva1 Larva1 Egg Egg Larva1 Egg Egg Egg Egg Larva1 Larva1
Egg Larva1 Larva1 Larva1 Egg Larva1 Larva1 Larva1 Larva1 Larva1 Egg Larva1 Larva1
Egg Larva1 Larva1 Larva1 Egg Larva1 Larva1 Larva1 Larva1 Larva1 Egg Larva1 Larva1
Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1
Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1
Larva1 Larva1 Larva2 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva2
Larva1 Larva2 Larva2 Larva2 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva1 Larva2 Larva2
Larva1 Larva2 Larva2 Larva2 Larva1 Larva2 Larva2 Larva2 Larva2 Larva2 Larva1 Larva2 Larva2
Larva1 Larva2 Larva2 Larva2 Larva1 Larva2 Larva2 Larva2 Larva2 Larva2 Larva1 Larva2 Larva2
Larva2 Larva2 Larva3 Larva2 Larva2 Larva2 Larva2 Larva2 Larva2 Larva2 Larva2 Larva2 Larva3
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Larva4 Larva4 Larva4 Larva4 Larva4 Larva4 Larva4 Larva4 Larva4 Larva4 Larva4 Larva4 Larva4
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0 0 0 0 0 0 0 0 0 0 0 0 0
0 18 0 10 0 0 0 0 0 0 0 18 0
0 38 0 54 0 0 0 0 0 0 0 38 0
0 37 32 33 0 0 12 0 0 0 0 37 32
28 46 45 16 16 18 35 0 0 0 28 46 45
29 26 48 13 18 40 21 0 0 0 29 26 48
18 28 51 65 57 54 7 15 36 21 18 28 51
34 11 37 23 48 58 0 24 32 27 34 11 37
27 23 56 25 54 45 Dead 56 36 18 27 23 56
23 26 27 24 52 33 Dead 48 57 14 23 26 27
19 13 20 25 43 26 Dead 42 55 19 19 13 20
27 14 25 12 40 23 Dead 37 43 17 27 14 25
34 22 23 17 35 26 Dead 29 40 38 34 22 23
23 26 16 22 31 24 Dead 36 38 42 23 26 16
26 52 18 28 38 17 Dead 52 33 34 26 52 18
20 22 14 19 35 21 Dead 48 21 35 20 22 14
14 35 15 22 22 20 Dead 33 25 21 14 35 15
11 16 12 47 17 16 Dead 16 15 13 11 8 12
6 11 9 35 14 12 Dead 9 17 3 6 0 9
3 7 6 18 11 10 Dead 3 12 7 3 Dead 6
0 2 3 6 9 6 Dead 0 11 5 0 Dead 3
0 1 0 3 6 3 Dead 0 9 0 0 Dead 0
Dead 0 0 1 8 0 Dead 0 5 0 Dead Dead 0
Dead 0 0 0 4 1 Dead Dead 2 0 Dead Dead 0
Dead Dead Dead 0 1 0 Dead Dead 0 Dead Dead Dead Dead
Dead Dead Dead 0 0 0 Dead Dead Dead Dead Dead Dead Dead

Figure 6: Life table data file dealing with only female. The main difference here to Figure 3 is that all individual that evolved and became male are not accounted for, the file only shows immature life stage ("egg", "larva", or "pupa", is recorded for each evaluation time.

II. ILCYM APPLICATIONS

2.1 System requirements

To be able to run ILCYM software you need to have Java and R programs installed in your computer; all these programs are embedded in ILCYM CD. Usually JAVA is automatically installed at the same time with ILCYM root platform; R and its libraries are installed manually. All packages and programs required by ILCYM are included in the CD or in zipfile on the following routes: "CD:\\Requirements\\ or may be downloaded from the website below. https://research.cip.cgiar.org/confluence/display/ilcym/Downloads

In case you have downloaded the software, make sure you unzip the requirements file and place the full package on your desktop before starting the installation.

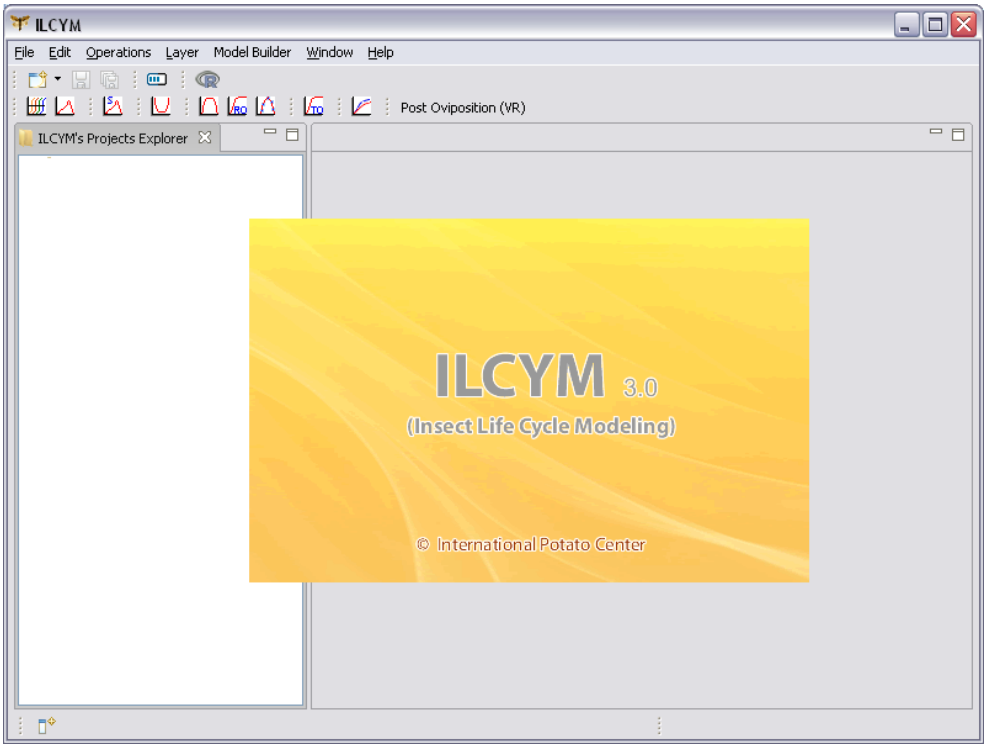
2.2 Installing ILCYM

2.2.1. Window XP operating system for computer with 32 bytes

To install ILCYM software in this operating system, the following steps need to be executed.

1. Double click in the INSTALL icon.
2. Select the route where the software will be installed (generally in **C:**Program files).
3. Follow the instructions.

Once the application has been installed, you will see the following window:



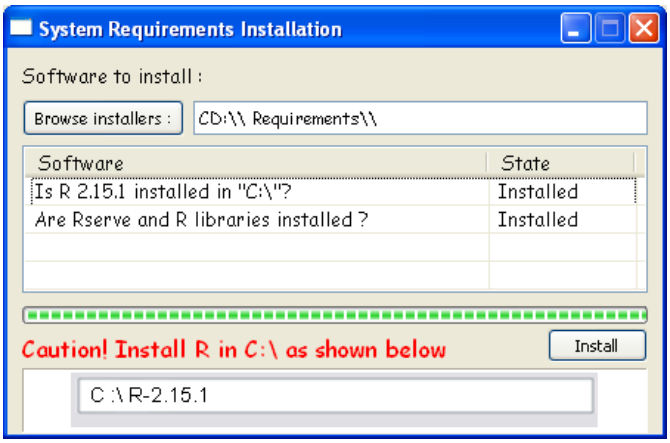
2.2.2 Windows Vista, 7 and above for computer with 32 bytes

1. Right click on the installer icon
2. Click on properties
3. Click on compatibility
4. Select the box compatibility mode
5. Select window XP (you may jump this step, the computer will automatically locate the appropriate window pack compatible for ILCYM)
6. Click ok
7. Select the route where the software will be installed.
8. Follow the instructions

When the application is launch click on the R symbol in the toolbar as shown below;

a window will appear indicating that the requirements have not been installed.

To load the applications, select the path where the installers are located (it maybe on the CD or in your desktop), select the items (one by one) and click the button *Install* to start your installation.

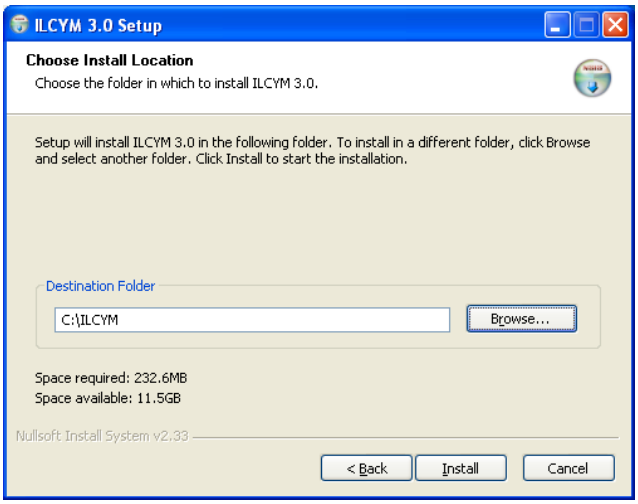


2.2.3 Windows Vista, 7 and above for computer with 64 bytes

To install ILCYM software in this operating system, you must follow the instructions listed below:

1. Double click in the INSTALL icon.

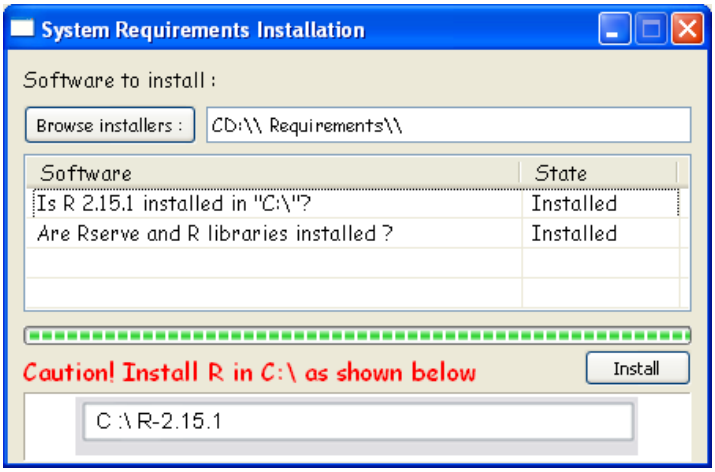
2. Instal ILCYM directly in **C:** as shown below


ILCYM 3.0 Setup
Choose Install Location
Choose the folder in which to install ILCYM 3.0.
Setup will install ILCYM 3.0 in the following folder. To install in a different folder, click Browse and select another folder. Click Install to start the installation.
Destination Folder
C:\ILCYM
Browse...
Space required: 232.6MB
Space available: 11.5GB
Nullsoft Install System v2.33
< Back
Install
Cancel

3. Follow the instructions and continue your installation until the end.

Note: For all window operating systems

1. Make sure the R-2.15.1 software is installed directly in **C:** as shown in the window below



2. Sometimes ILCYM users miss to correctly follow some steps during the software installation process and when starting to run the software, the following error message appears "***not connecting to R***". To remedy you should follow the instructions below:

Steps A: Completely remove ILCYM and R in your computer

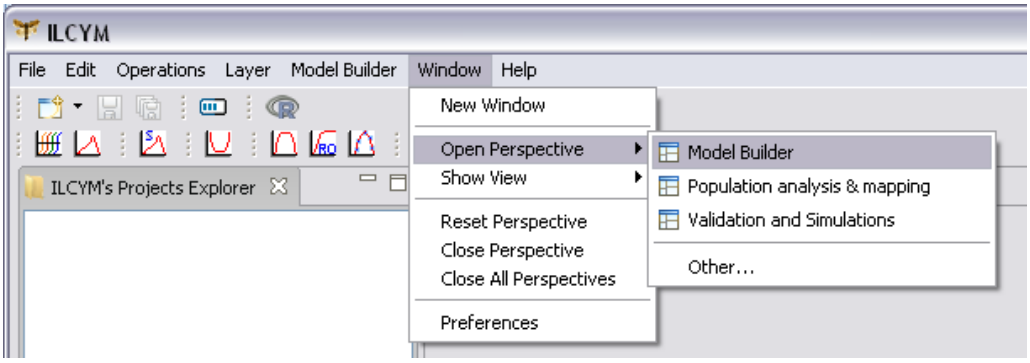
1. Go to control panel, click on add/remove program,
2. Click on remove program and uninstall ILCYM,
3. Still on add/remove program, click on R and uninstall R
4. Go to my computer, click on **C: \,** then program file, (in case you are using window operating system with two program files (one for 32 bites and the other for 64 bites)), check both folders and complete delete ILCYM

5. Go to my computer against, click **C: \,** and then delete the R folder.

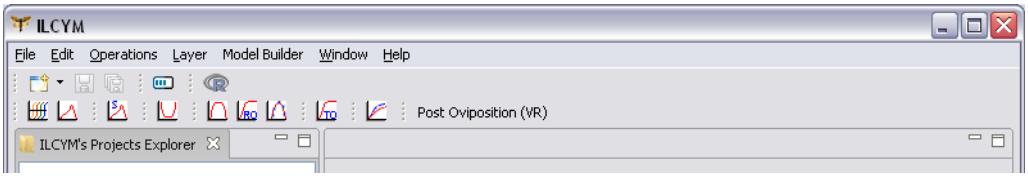
Steps B: Reinstall at fresh ILCYM by carefully following the instruction in section 2.2 of this manual.

III. ILCYM'S PERSPECTIVES

This latest version of ILCYM software is made of perspectives. A perspective is a collection of views and actions, which are useful for specific tasks for users. ILCYM 3.0 contains 3 perspectives: **Model Builder**, **Validation & Simulation** and **Analysis of mapping population**. To access the outlook of a perspective, go to **menu Window** -> **Open Perspective** and **Select** the perspective you want to use.



3.1 Model Builder



ILCYM's model builder is a complete modeling interface that helps the software users to develop insect phenology model (IPhM). Some of its key features include:

- The wizard that automates the creation of new life stage processes or the editing of existing processes.
- The property sheets that let the user to quickly modify the properties of input data, sub-model and produce the overall phenology model.
- The model window where user build and save the developed models

- Layout tool that help the user to neatly arrange the IPhM
- The entire IPhM is saved in HTML file to enable user to easily share or export for reports and publications write-up.

The model builder in ILCYM helps the user to build, manage, and automate phenology models. Without model builder, the management of models and the data supporting them can be difficult. Phenology models contain a number of interrelated life stage processes and with the model builder ILCYM user can at any time, add, replace or delete sub-models. In addition, users can replace old data with new information, change assumptions as well as model parameters, and consider alternatives sub-model combinations. In summary ILCYM model builder is a flexible interface for creating, visualizing, running, modifying, documenting, and sharing models.

- ***Create phenology Model*:** The user creates a phenology model by adding sub-models. Each life stage has a wizard – a sequence of dialog boxes that prompts user's for the information needed to define the stage process and then add the process to the over all phenology model.
- ***Visualize phenology model:*** Data, life stage sub-models, and their choosing parameters are symbolized in the window named "summarize". In this window, user can visualize the flow of processing in the phenology model building and see which life stage are included in an analysis and which possible output is created from which input.
- ***Run model:*** The Model Builder runs the sub-models that make up the over all phenology model. It creates the output data sets, saves them to the software workspace and loads them as object for simulations and mapping.
- ***Modify phenology model:*** Every section in a life stage process has property sheets that contain all information about the sub-model (mathematical expression, parameters, reset bottom, etc.). For example, by resetting a selected sub-model, user can modify component of their over phenology model and explore alternative outcomes.

- ***Document phenology model:*** ILCYM's model builder provides text boxes in which user can documents the methods of data collection, different assumptions made during model development. The documentation informs other users on how the model was built, what assumption was made, and what result was obtained.

Share produced phenology model: ILCYM's user can share phenology model by sharing the model files created in the model builder. All created file during model development are automatically store in the workspace. In doing that, it let users to open the methodology for wide scrutiny and helps refine and standardize modeling techniques. Sub-models can be imported, allowing users to incorporate components that have been developed by others into their own models.

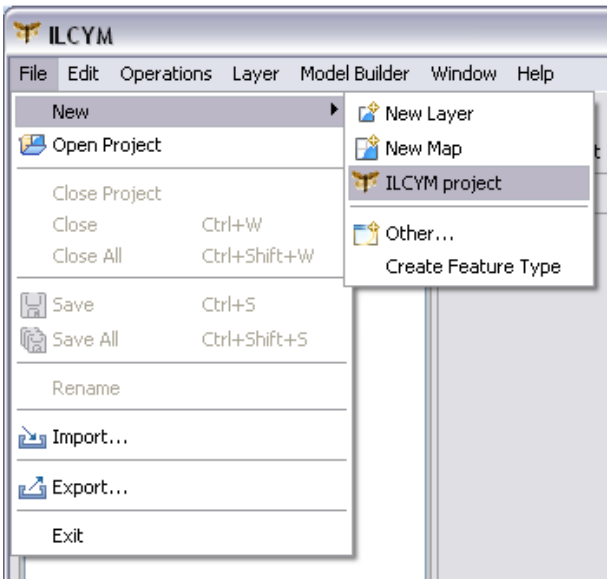
3.1.1 Creating new project

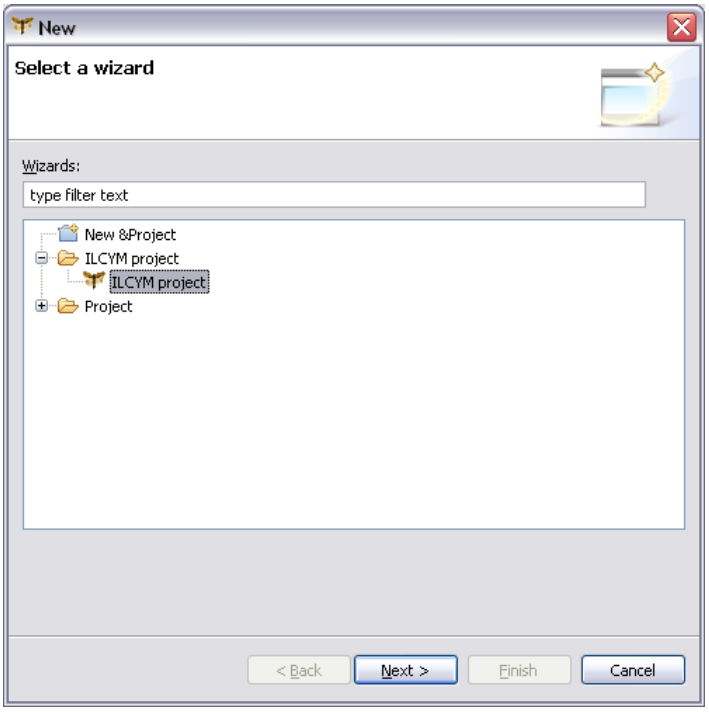
Before you start with an evaluation of data for developing an insect phenology model, you need to create and register a new project. All data, evaluation outputs, maps, etc. that are used or created during project development are managed within a single "ILCYM's project".

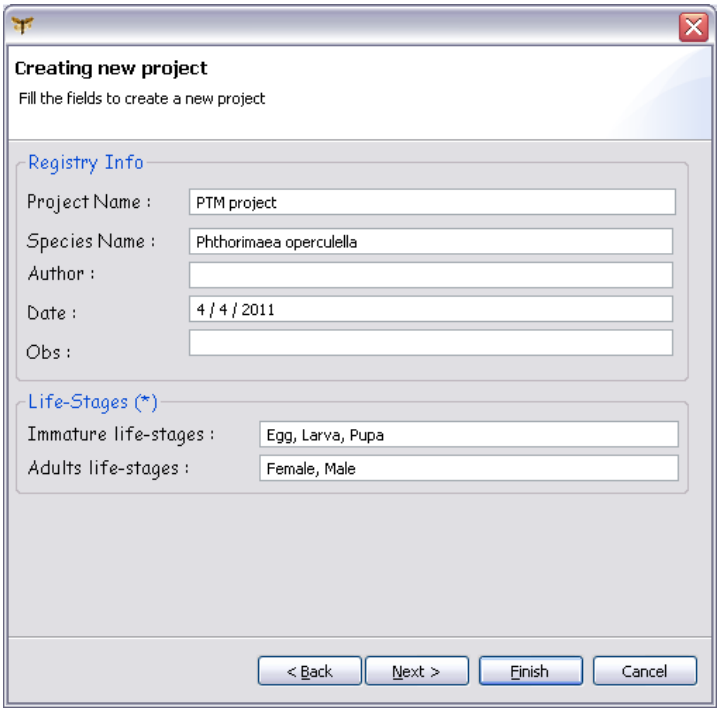
Therefore for each insect species you want to develop a model, a new project needs to be created. To create a project follows the steps below:

Go to **File Menu** -> **New** -> **ILCYM Project**.

Note: The first two options in the "New" sub-menu refer to creating a new uDig project which should not be confused with an ILCYM project.


ILCYM
File
Edit
Operations
Layer
Model Builder
Window
Help
New
Open Project
Close Project
Close Ctrl+W
Close All Ctrl+Shift+W
Save Ctrl+S
Save All Ctrl+Shift+S
Rename
Import...
Export...
Exit
New Layer
New Map
ILCYM project
Other...
Create Feature Type

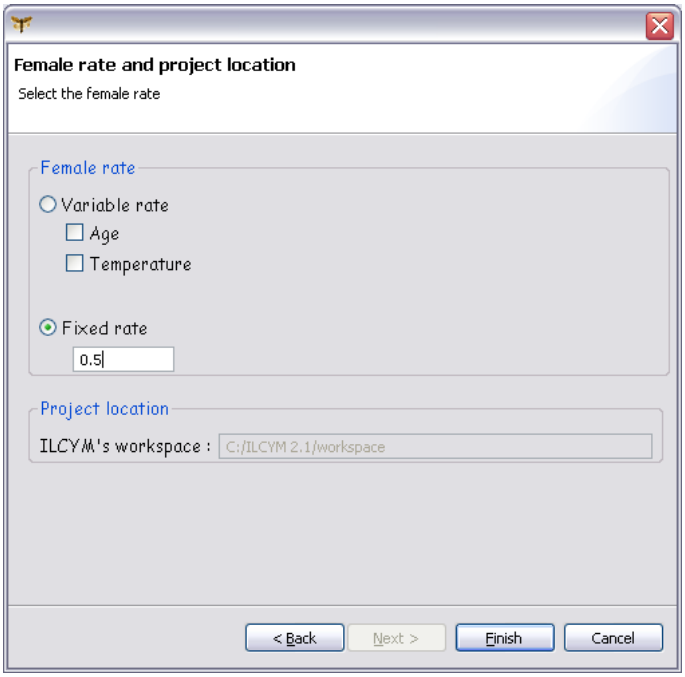

New
Select a wizard
Wizards:
type filter text
New &Project
ILCYM project
ILCYM project
Project
< Back
Next >
Finish
Cancel



(*) Means that the fields must be obligatorily filled; user should input all the development stages of the insect that S/He will be evaluating separated by a comma (,). For complete life-table data, the user must write the life-stages as it is written in the data files (note that ILCYM's is character case sensitive). For Adults stages by convention, you need to write start with "**Female"** and then "**Male**" stages. If you forgot one or more life-stages, after creating the project you need to delete that project and create a new project.

The functions used in creating a project are well described below.

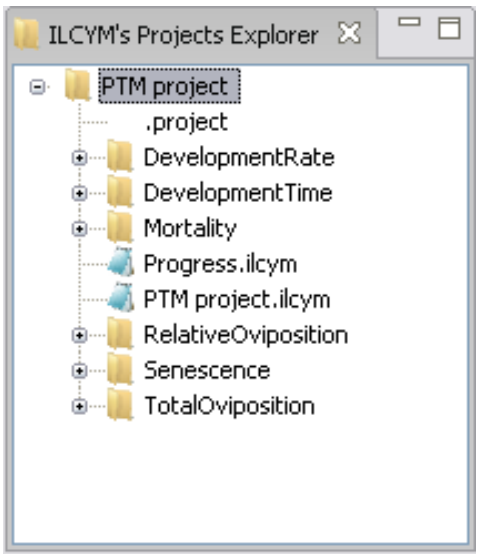
- ***Project Name***, Name of the Project.
- ***Species Name***, Write the name of the species
- ***Autho****r*, Name of the person creating the project.
- ***Date*****,** Date of the project creation (it appears automatically).
- ***Observations***, Here author might include some experimental observations (temperature, RH, other conditions, problems, etc.) or general note that s/he is important to the project under creation.
- ***Immature life-stages***, Stages need to include all life stages describing the whole life cycle of the insect species; i.e. Egg, Larva, (Prepupa,) Pupa (or: E, L, (PP,) P). Larval stages might be separated in different instars if required (p.e. L1, L2, L3, etc.; or nymph1, nymph2, etc.).
- ***Adult's life-stages***, Insect matures life-stages ("F" for Females, "M" for Males).



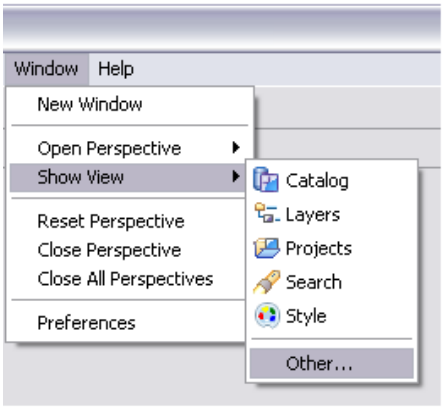
- ***Age***, Check this button if you know that the female rate in the progeny is changing with adult female age. In this case a new function will be included in the overall model that determined the age-depended oviposition curve.
- ***Temperature***, Check this option if you are dealing with species that the temperature has an influence on the female rate in the progeny. In this case a new function will be included in the overall phenology model that determined the temperature-depended oviposition curve.
- ***Fixed Rate***, If the female rate is expected to be constant, i.e. independent of the temperature and female age, or any other parameter, mark this button and indicate the value of female rate, usually 0.5.

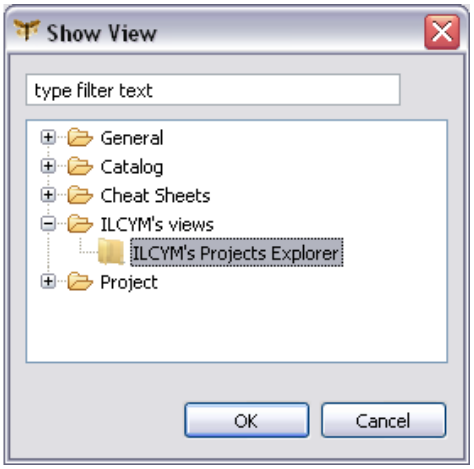
In all situations, one button needs to be checked, other wise the project registrations will fails (i.e. the wizard does not switch to the next step). If the female rate in the progeny is well known from previous studies, to be constant over all temperatures, and independent from the age of ovipositing females, then it is recommended to check both buttons.

All projects will be saved in the workspace created automatically during the software installation, and will be displayed in ILCYM project explorer view.



If the ILCYM project view does not appear go to ***Window menu*** -> ***Show view*** -> ***Other*** then expand "**ILCYM views**" and click in "**ILCYM project explorer**".



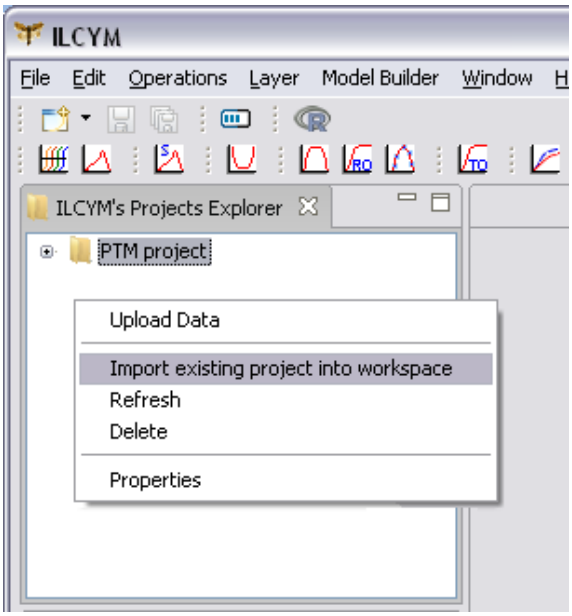


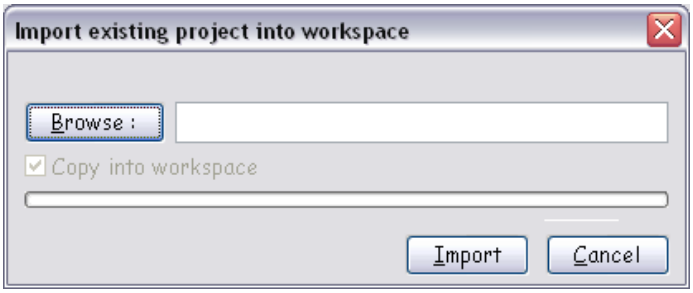
3.1.2 Importing project

If you have created a project and you want to display or work on it in another computer, the complete project should be imported into the ILCYM workspace.

This is because; when a project is created the file paths are saved and should be updated when transferring the project in a new computer.

To import the project right click in ***Project Explorer* view** and click on ***Import existing project into workspace***.

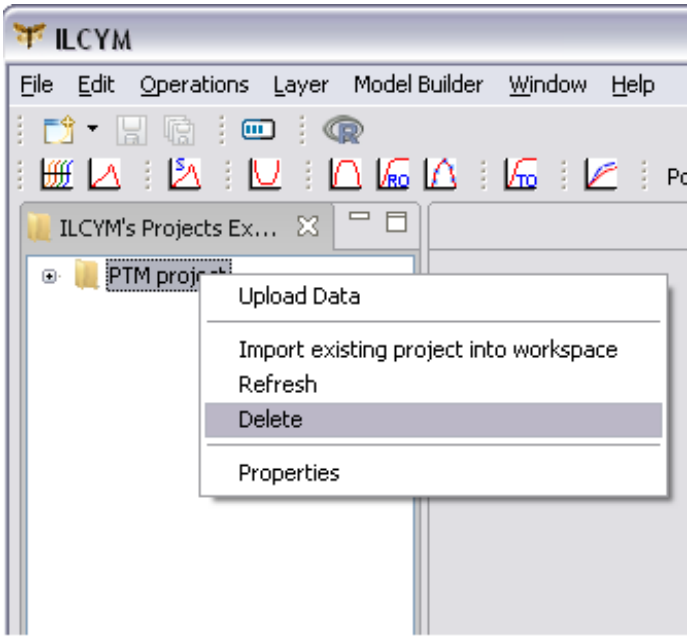




A window will appear, click on ***Browse* button** to look for the project to import and then click on ***Import* button**

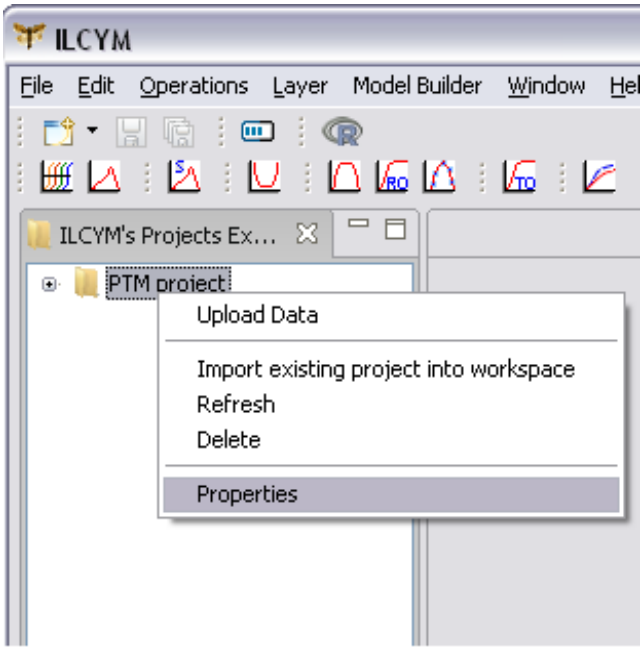
3.1.3 Deleting project

During project creation, if the user has forgotten some life-stages and desire to delete the project and create a new project, s/he must ***right click on the project*** and select ***Delete* option**.



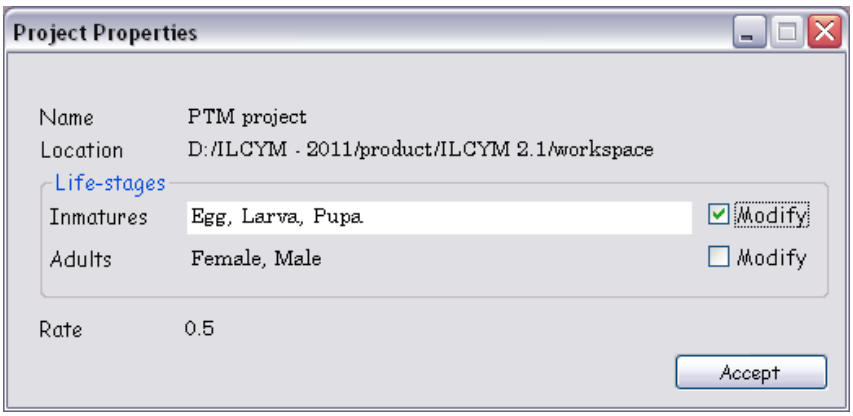
3.1.4 Project Properties

To view a project summarize of life-stage, path and rate just ***right click on the project*** and select ***Properties option***.



If the user has entered a wrong spelling for a life stage (different on how it is writing in input data file i.e *LarvA* instead of *Larva*), this can be changed by

enabling the option ***Modify*** and then clicking on the button ***Apply*****.** This is because ILCYM objects are case sensitive

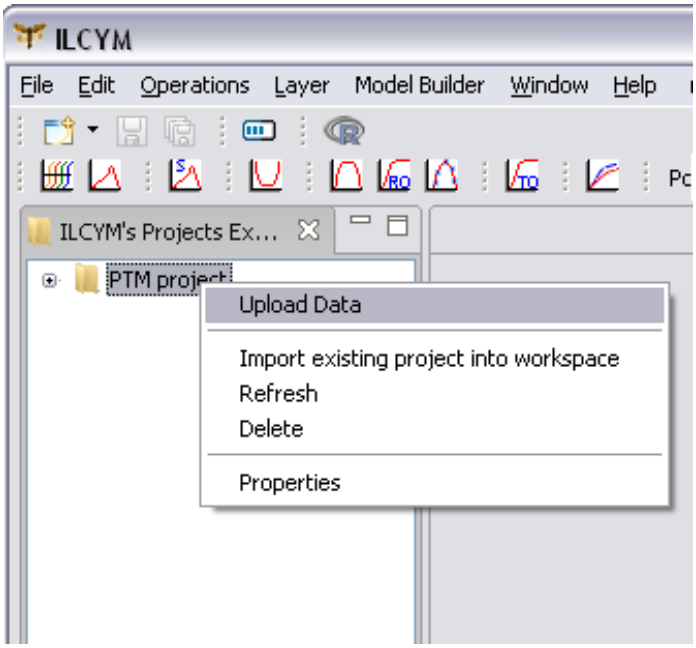


Note: Within this window you can change the spelling of the any immature stages, but you can not increased or reduce the number of stages. In case the number of stages in your created project is not conforming to the number of stage in your data, we recommend you to create a new project.

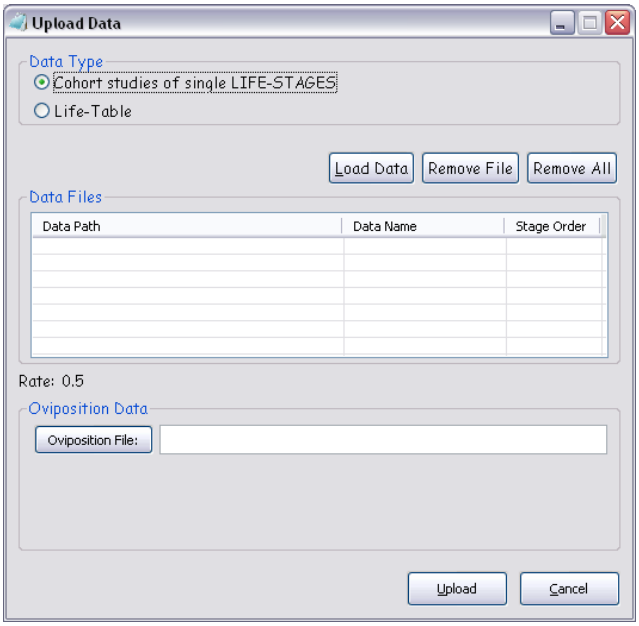
3.1.5 Uploading data

For demonstrating how to manipulate data in ILCYM we used the collected data of the potato tuber moth, *Phthorimaea operculella* Zeller, as an example in this manual. The data is described in Sporleder et al. (2004). The phenology model for this specific pest is already established and it can be use for modeling studies including risk mapping for spatial simulation of *P. operculella* for a specific region or zone of interest described later in this manual.

Once the project is registered you might upload the files containing the (experimental) data used to determine the model functions. **Right click on the project** and **click in *Upload Data***.



Indicate the type of data to be evaluated (for example data "Cohort studies" need to be chosen) and browse for the data files by clicking on "**Load data**". After a ***left mouse-click on a file*** (browse window, right) the file appears in the "upload window". Include only the data that are used to determine development times and mortalities in immature life stages and survival times of adults. For modeling reproduction an extra oviposition file is required that need to be uploaded specifically.



a) Uploading cohort data

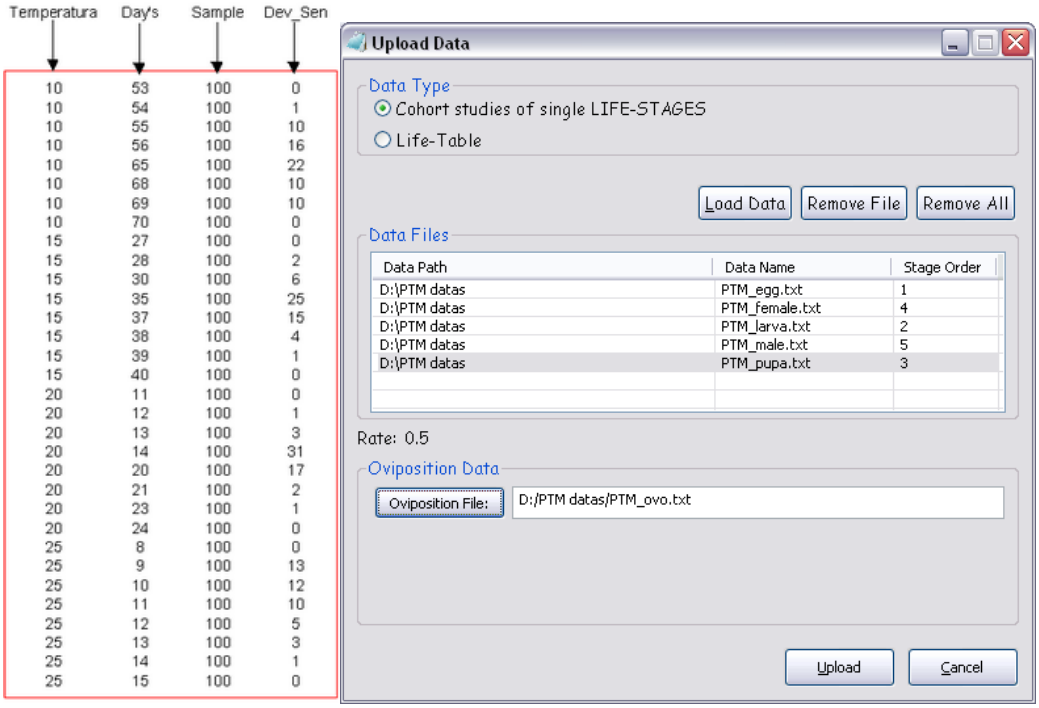
Data for all temperature experiments from one life stage are included in one file; i.e. one file for each specific life stage. It is recommended to name the file according to the "Species name" and the "specific life stage" for easy identification (p.e. "PTM_egg", "PTM" for potato tuber moth and "egg" for the egg-life stage. The files should be saved as "**.txt**"-files. The data are sorted according to:

1. The temperature (first column).

2. The number of days observed for the development time or senescence in adult (second column).

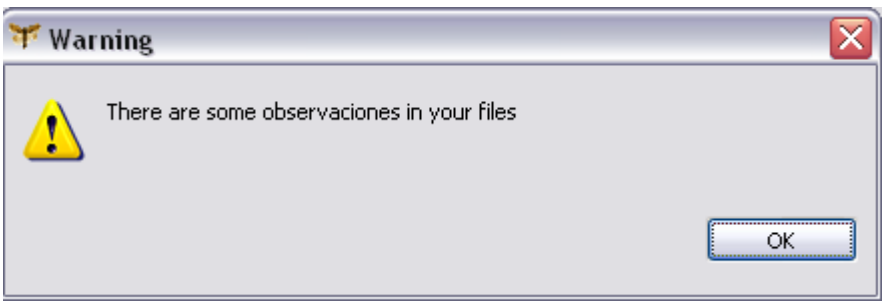
3. Number of insects in the sample (cohort) (third column).

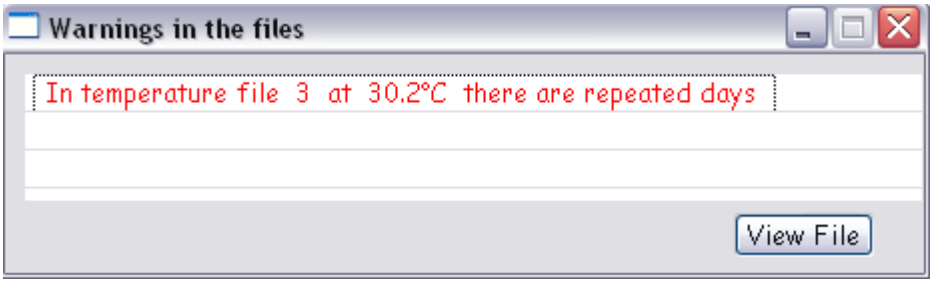
4. The number of individuals that developed to the next stage on this particular day (fourth column).



Chosen data files appear in the data file list (file location, file name, and order of particular stage that the data are representing is indicated). The "**Stage Order**" is placed automatically in the sequence in which the data were uploaded, however you are requested to rearrange the order following the order in which you have declared your life stages (If you started with egg following by larva, the file with egg should be **1** and larva **2**). You change the order by clicking the "**Stage Order**" number and changing the value manually.

ILCYM before uploading files, check for possible problems and highlight them. When Clicking on ***View* button** ILCYM shows the file with errors that can be solve through ILCYM interface.

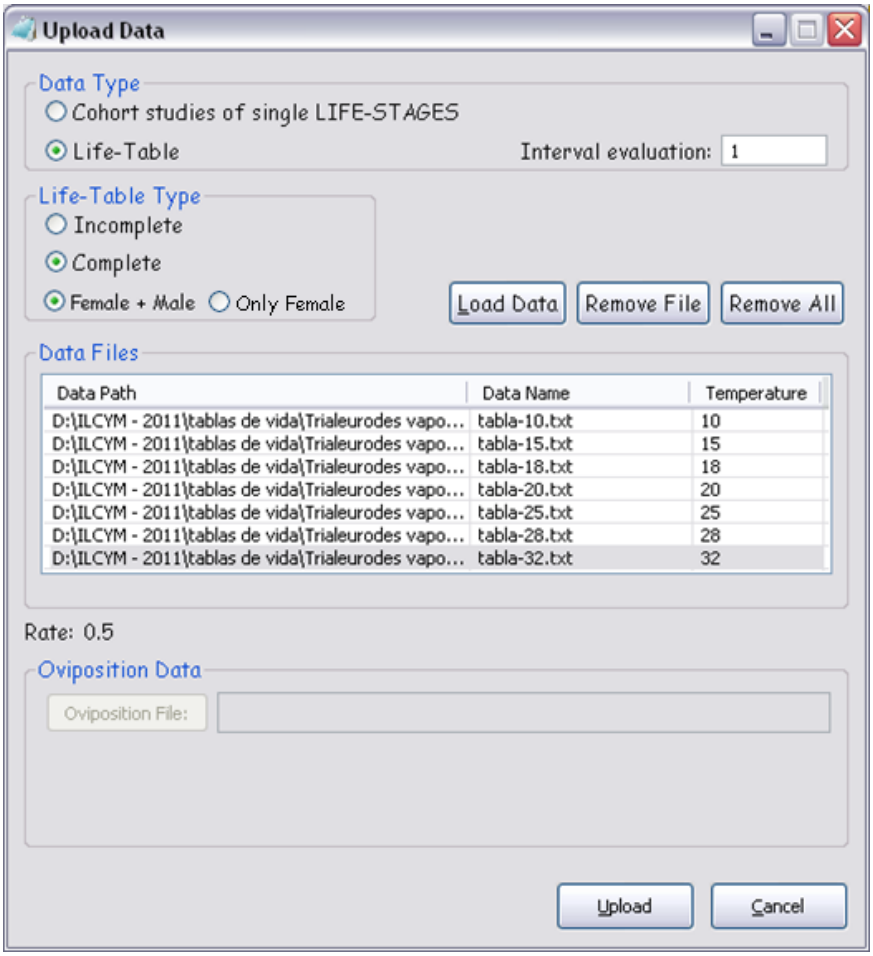




b) Uploading life-table data

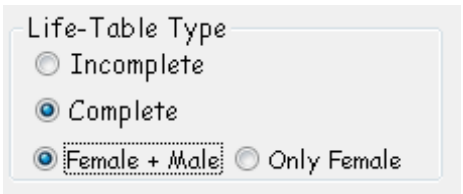
A life-table tracks the history of an insect cohort, generally starting from "eggs", i.e. it shows the life history of each individual of the cohort (in columns). The state of all individuals is noted daily (rows) until the last individual of the cohort has died. For each individual surviving the development stage (in the sample below: Egg, Larva, and Pupa) is noted; non-survivors are marked (i.e. "Dead"). In the case of male adults "Male" is entered while for living female adults the number of oviposited eggs is noted. This is a complete life-table. The life-table would be incomplete if the cohorts' history was followed-up until the insects have reached the adult stage (i.e. incomplete life-table). In this case additional data about oviposition from additional experiments (p.e. another group of adult insects) are required; called "oviposition file" (see below). When using/uploading "complete life-tables, the "oviposition file" is generated automatically from the data.

	Insect 1	Insect 2	Insect 3	Insect 4	Insect 5	.....
Day 1	Egg	Egg	Egg	Egg	Egg	
Day 2	Egg	Egg	Egg	Egg	Egg	
Day 3	Egg	Egg	Dead	Egg	Egg	
Day 4	Larva	Larva	Dead	Larva	Larva	
Day 5	Larva	Larva	Dead	Larva	Larva	
Day 6	Larva	Larva	Dead	Larva	Larva	
Day 7	Larva	Larva	Dead	Dead	Larva	
Day 8	Larva	Larva	Dead	Dead	Larva	
Day 9	Pupa	Pupa	Dead	Dead	Larva	
Day 10	Pupa	Pupa	Dead	Dead	Pupa	
Day 11	Pupa	Pupa	Dead	Dead	Pupa	
Day 12	Pupa	Pupa	Dead	Dead	Pupa	
Day 13	Pupa	Pupa	Dead	Dead	Pupa	
Day 14	Pupa	Male	Dead	Dead	Pupa	
Day 15	32	Male	Dead	Dead	Dead	
Day 16	25	Male	Dead	Dead	Dead	
Day 17	5	Male	Dead	Dead	Dead	
Day 18	7	Male	Dead	Dead	Dead	
Day 19	1	Male	Dead	Dead	Dead	
Day 20	0	Male	Dead	Dead	Dead	
Day 21	0	Male	Dead	Dead	Dead	
Day 22	Dead	Dead	Dead	Dead	Dead	



Here is an example of a file that includes the data for all insects at one specific temperature. It is recommended to include the temperature in which the life-table was established in the file-name for easy identification; p.e. "PTM-20.txt"; "PTM" for potato tuber moth and "20" indicates the temperature 20°C in which the life-table was established. The user must indicate the interval of evaluation of S/He project, if the evaluation is daily write 1(one) if is twice per day write 0.5

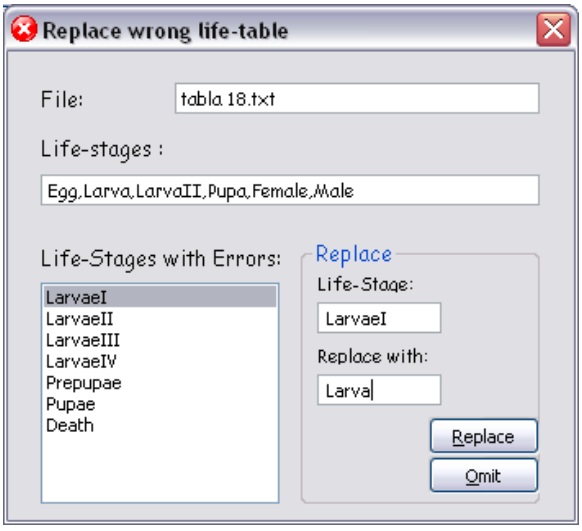
For complete life table, distinction has been made for data that contain both female and male or only female information. The user only needs to choose complete and select one of the options



For variable rate it is require that the user uploads 2 oviposition files, one for female and the second for male. These files must also include the *Dead label* p.e. “Dead”, “Death” depending on how it appeared on the data file.

If the files contain life-stages with different names from what were initially registered, ILCYM recognizes the errors and displays appropriate names for replacement.

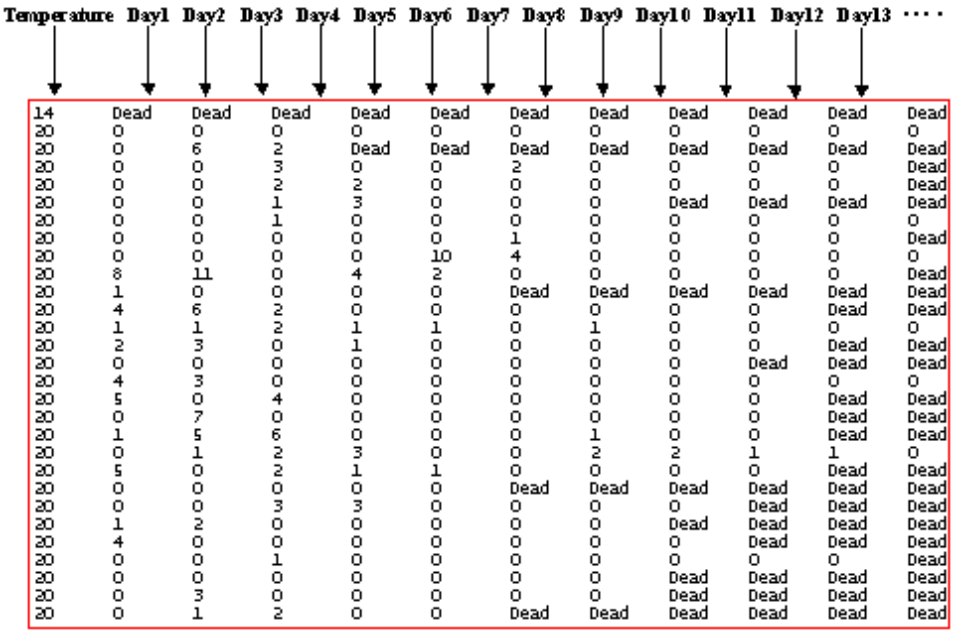
Dead label, marks the difference between the stages that the insect dies which is writing in the data “**Dead**” or “**Death**” from the stage that the insect still alive but did not lay egg replace by “**zero” =** “**0**”.



In this example the user wrote “Egg, Larva, LarvaII, Pupa, Female, Male” and ILCYM evaluates each files and look for different names, which are “LarvaeI, LarvaeII, ,LarvaeIII, LarvaeIV, Prepupae, Pupae”, the user must select one by one and write the correct name in *Replace with* text box and click on *Replace* button, only the word “Death” must be omitted.

c) Oviposition file

If oviposition is not included in the life-table files (incomplete life-table) or if data were individually collected for specific life stages (cohort-studies), then an oviposition file is required for modeling reproduction for the insect species. An example of data is given below where, each row in the file represents an individual female. The first column indicates the temperature in degree C to which the female was exposed. The following row represents the day post adult emergence and the values represent the "number of eggs" oviposited at a particular day. If females were tested in groups' average number of eggs per female should be recorded for each repetition.



Temperature	Day1	Day2	Day3	Day4	Day5	Day6	Day7	Day8	Day9	Day10	Day11	Day12	Day13	....
14	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	
20	0	0	0	0	0	0	0	0	0	0	0	0	0	
20	0	6	2	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	
20	0	0	3	0	0	2	0	0	0	0	0	0	Dead	
20	0	0	2	2	0	0	0	0	0	0	0	0	Dead	
20	0	0	1	3	0	0	0	0	Dead	Dead	Dead	Dead	Dead	
20	0	0	1	0	0	0	0	0	0	0	0	0	0	
20	0	0	0	0	0	1	0	0	0	0	0	0	Dead	
20	0	0	0	0	10	4	0	0	0	0	0	0	0	
20	8	11	0	4	2	0	0	0	0	0	0	0	Dead	
20	1	0	0	0	0	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	
20	4	6	2	0	0	0	0	0	0	0	0	Dead	Dead	
20	1	1	2	1	1	0	1	0	0	0	0	0	0	
20	2	3	0	1	0	0	0	0	0	0	0	Dead	Dead	
20	0	0	0	0	0	0	0	0	0	0	Dead	Dead	Dead	
20	4	3	0	0	0	0	0	0	0	0	0	0	0	
20	5	0	4	0	0	0	0	0	0	0	0	Dead	Dead	
20	0	7	0	0	0	0	0	0	0	0	0	Dead	Dead	
20	1	5	6	0	0	0	1	0	0	0	0	Dead	Dead	
20	0	1	2	3	0	0	2	2	1	1	1	0		
20	5	0	2	1	1	0	0	0	0	0	0	Dead	Dead	
20	0	0	0	0	0	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	
20	0	0	3	3	0	0	0	0	0	0	Dead	Dead	Dead	
20	1	2	0	0	0	0	0	0	Dead	Dead	Dead	Dead	Dead	
20	4	0	0	0	0	0	0	0	0	0	Dead	Dead	Dead	
20	0	0	1	0	0	0	0	0	0	0	0	0	Dead	
20	0	0	0	0	0	0	0	0	0	Dead	Dead	Dead	Dead	
20	0	3	0	0	0	0	0	0	0	Dead	Dead	Dead	Dead	
20	0	1	2	0	0	Dead	Dead	Dead	Dead	Dead	Dead	Dead	Dead	

If the individual dies, the user must indicate this status in the file by writing "**Dead**". This allows differencing between zero oviposition when the insect is alive and zero oviposition due the dead of the insect.

3.1.6 Developing the overall phenology

To obtain a full phenology of a particular species, the six (6) evaluations below are performed in subsequent order.

Name	Description
1. Development time and its variation	Fits the development curve in a parallel line assay to accumulated development frequencies of each constant temperature tested. The application delivers an estimate of the median development time (days) with the standard error (SE) at 95% Confidence Limits for each temperature, and a parameter describing the variation in development times between individuals.
2. Development rate	This parameter is obtained through fitting of various functions that describe the relationship between temperature and the development rate.
3. Senescence	The fitting of various functions that describe the relationship between temperature and the adults' senescence.
4. Mortality	The fitting of functions that describe temperature-dependent mortality is done and with the help of some statistical criteria, best model is selected.
5. Total oviposition	The total oviposition is obtained by fitting functions that describe temperature-dependent total oviposition per female.
6. Relative oviposition frequency	Fit a function to describe the age-dependent relative oviposition frequency curve. Depending on the settings, when a project is registered (see page 33) optionally functions for describing temperature-dependent and age-dependent female rates will be evaluated.

Note: For incomplete life table, two oviposition files are loaded as input data, a function representing female ration in the oviposition is estimated and added to the overall phenology model.

7. Female ration in the oviposition	Fit a function to describe the female ration in the oviposition.

In case where the female rate of the species under investigation is variable, a new evaluation "**Rate oviposition**" is conducted and included on the overall phenology model. Such addition will make the overall phenology model for a species to contain 7 functions.

8. Rate oviposition — Nonlinear function describing oviposition frequency of female

Post oviposition is also an additional evaluation that can be conducted for insect with variable rate; this represents the age-specific survival rate describing the proportion of the number of eggs alive at any given time.

9. Post oviposition — Stands for age-specific survival rate that described the proportion of number of eggs alive at any given age (time).

Note: The "**post oviposition**" evaluation is not included in the overall phenology model.

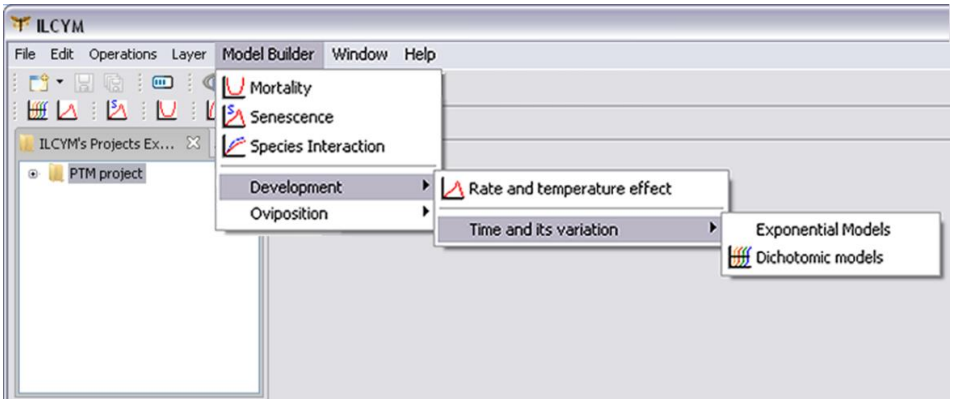
a) Development time and its variations

For conducting this evaluation ILCYM's software offers two options:

i) ***Using dichotomic models***: The data are fit to three binary distribution models (Logit, probit, and complementary log, CLL]). The user selects the best model based on added selection criterion such as the Akaikes selection criterion (AIC). On the basis of the selected function the "median development times" with 95% confidence limits are estimated (output statistics are explained on subsequent pages).

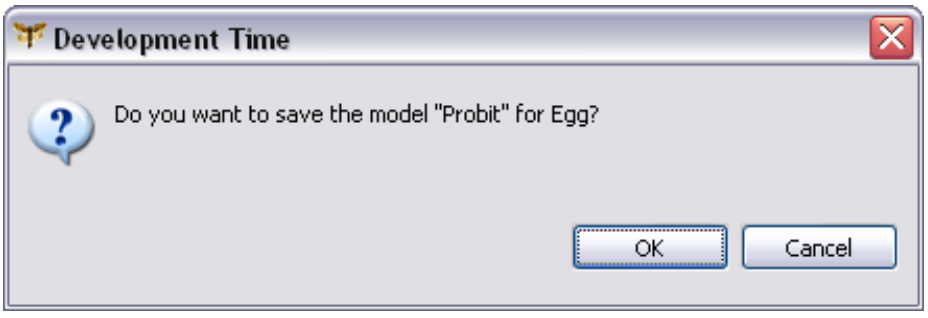
ii) ***Using exponential models:*** From the input data, a weighed median developmental time is estimated; the obtained values are normalized, and then plotted against the accumulated frequency at each temperature. The plotted points are fitted to a series of 6 exponential functions that include the gamma and weibull distribution functions. The user selects the best-fitting function according to ILCYM's inbuilt selections criteria, e.g. the Akaikes selection criterion (AIC). Using the best-fitted function, a global median developmental time is estimated, and then used to calculate individual media developmental time at each temperature.

The window below display how development time is estimated in ILCYM. Under ***Model Builder***, go to ***development***, select ***Time and its variation*** and then choose one of the options: ***Exponentia Models*** or ***Dichotomic Model*** and then proceed with your analysis.

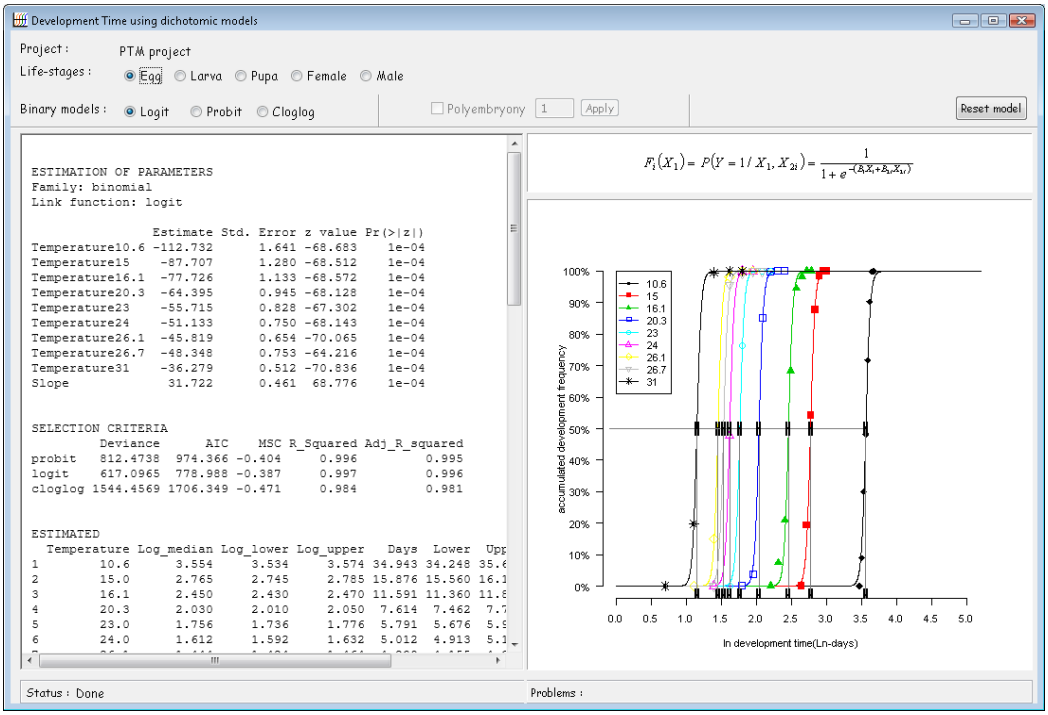


Once an option is chosen, the user is requested to the select the insect life stage and the analysis will start automatically and this will provide a statistical outputs, a mathematical expression of your selected distribution function and a figure showing the data points entered in the analysis and the resulting development frequency curves for each temperature.

After the calculation this window will appears, to proceed, click ***Ok*** **button** if you **agree** to the selected function or ***Cancel*** and select another function based on the model selection criteria.



If the user wants to change a model already selected, just click on ***Reset*** **button** and click the life-stage for reevaluation.


Development Time using dichotomic models
Project : PTM project
Life-stages : Egg Larva Pupa Female Male
Binary models : Logit Probit Cloglog
Polyembryony 1 Apply
Reset model
ESTIMATION OF PARAMETERS
Family: binomial
Link function: logit
Estimate Std. Error z value Pr(>|z|)
Temperature10.6 -112.732 1.641 -68.683 1e-04
Temperature15 -87.707 1.280 -68.512 1e-04
Temperature16.1 -77.726 1.133 -68.572 1e-04
Temperature20.3 -64.395 0.945 -68.128 1e-04
Temperature23 -55.715 0.828 -67.302 1e-04
Temperature24 -51.133 0.750 -68.143 1e-04
Temperature26.1 -45.819 0.654 -70.065 1e-04
Temperature26.7 -48.348 0.753 -64.216 1e-04
Temperature31 -36.279 0.512 -70.836 1e-04
Slope 31.722 0.461 68.776 1e-04
SELECTION CRITERIA
Deviance AIC MSC R_Squared Adj_R_squared
probit 812.4738 974.366 -0.404 0.996 0.995
logit 617.0965 778.988 -0.387 0.997 0.996
cloglog 1544.4569 1706.349 -0.471 0.984 0.981
ESTIMATED
Temperature Log_median Log_lower Log_upper Days Lower
1 10.6 3.554 3.534 3.574 34.943 34.248
2 15.0 2.765 2.745 2.785 15.876 15.560
3 16.1 2.450 2.430 2.470 11.591 11.360
4 20.3 2.030 2.010 2.050 7.614 7.462
5 23.0 1.756 1.736 1.776 5.791 5.676
6 24.0 1.612 1.592 1.632 5.012 4.913
10.6
15
16.1
20.3
23
24
26.1
26.7
31
accumulated development frequency
ln development time(Ln-days)
Status : Done
Problems :

Line 1: indicates adjusted model family

Line 2: indicates the best-fitted model

Block of lines below line 2: Intercepts for each temperature, standard error (SE), z-values, and the probability. The last line of the block shows the common estimated slope, these parameters all describe variation of the development time at different temperatures.

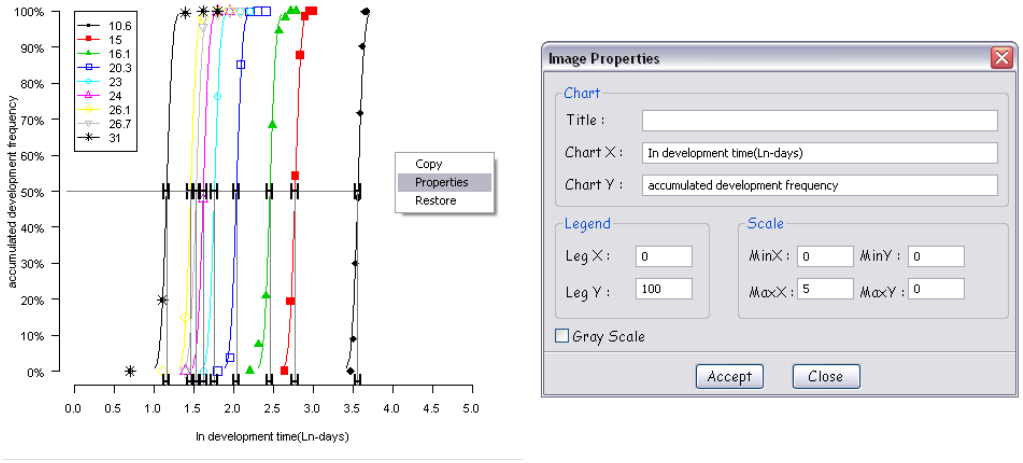
Selection criteria

Lists of criteria used to select one out of many provided functions or models. The most important are the AIC that demonstrates the deviations between observed and predicted data (MRC is an extension of AIC) and the R^2 that explains how the model captures the variability within the data.

To modify the scales, legend's coordinates titles of the graphs **click** on the **properties** in the popup menu of the image.

To visualize the changes **click** on the "**Accept**" button.

If you want to restore change only, **right click** on **Restore** option in the **menu**.

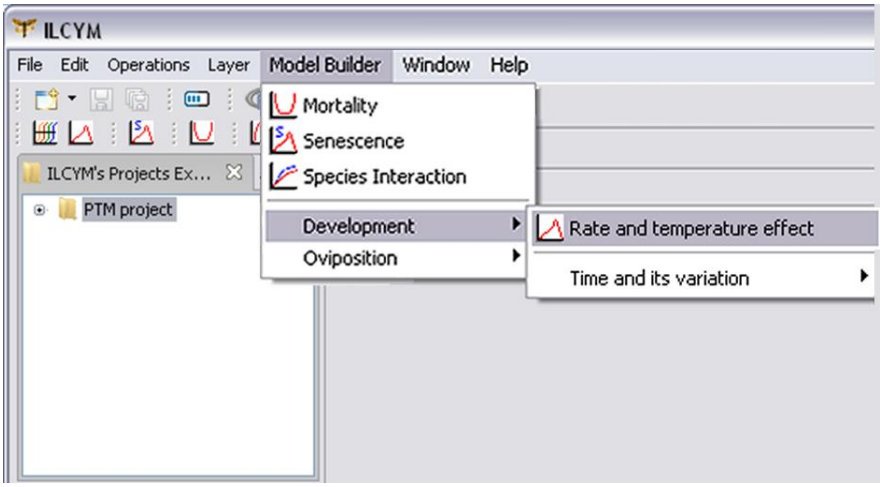


Copy option allows copying the image to the clipboard and then pasting in any other document.

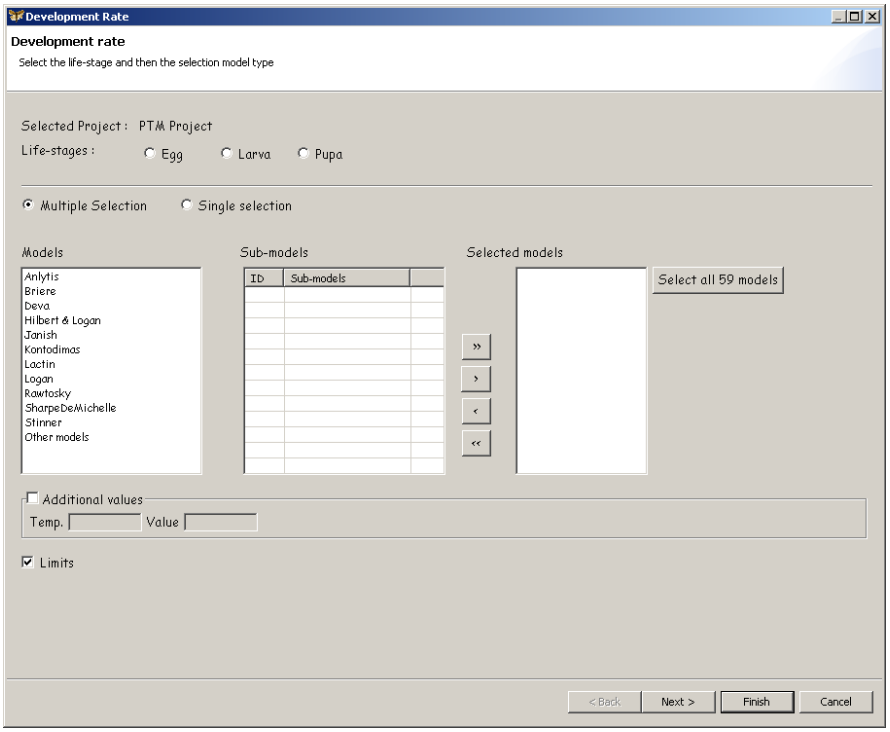
Restore option: restore the image to the original design.

b) Development rate

The inverse of the median time (1/median time), calculated by the estimated function of the development distribution is the development rate due to temperature. This evaluation in ILCYM complements the evaluation of the development time; here you fit a model that describes the temperature-dependent development rate for each particular life stage. ILCYM provides a number of models that might describe well the development curve of insects. ILCYM does not check the appropriateness of each model automatically. You might test several models and select the best one according to the selection criteria AIC and MSC.



ILCYM contains different models for development rate; these models are represented by the name of the first authors who first developed the equation i.e Shape De Michelle, Deva, Logan etc… Under the name of each author, there are series of models developed from the original equations marked by number i.e Shape De Michelle 1, Logan 2 etc.



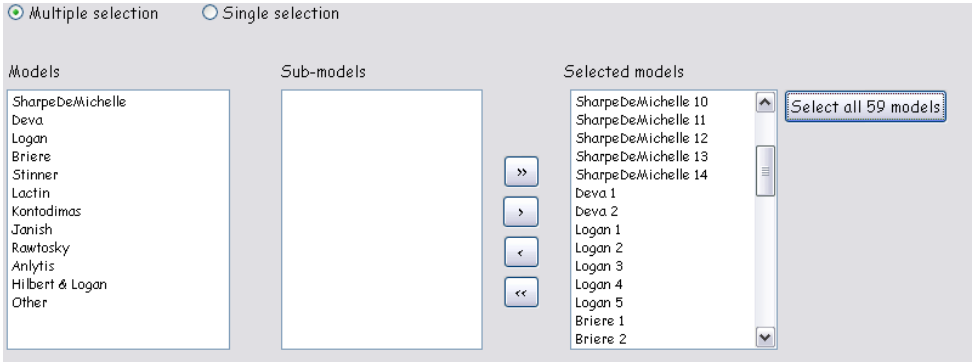
The first page of the wizard displays the name of the project and the stages that the user created during project development as well as options to select the

best model, either by comparing various sub-models or all at once or separately by choosing a sub-model.

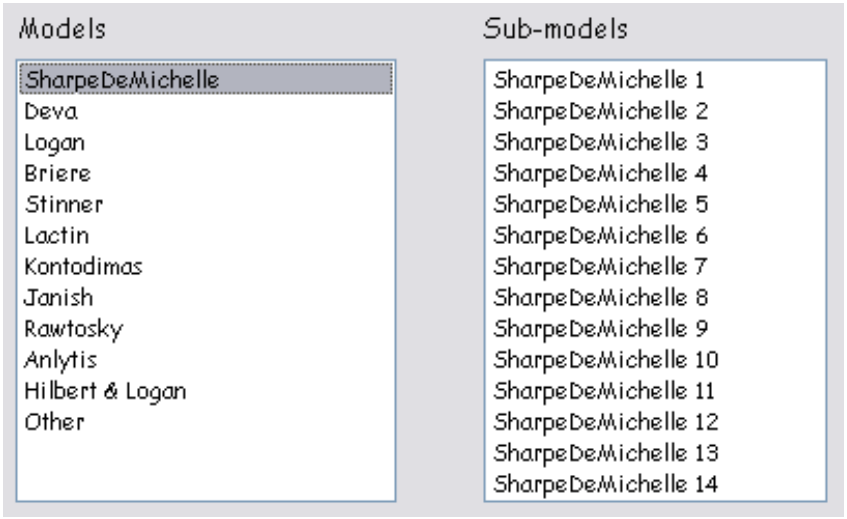
In this menu you can operate multiple selections or single selection

Multiple selections

i) Select all sub-models at once and choose the best fitted sub-model using inbuilt selection criteria.



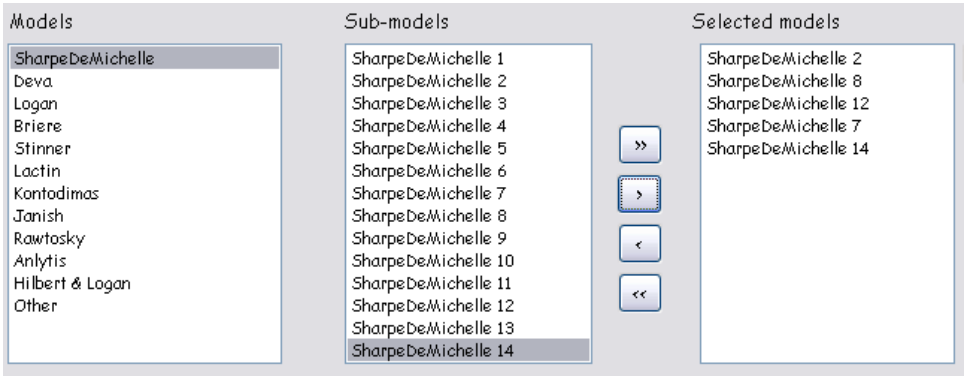
ii) Select a group of models i.e Sharpe De Michelle will displays all sub-models that originated from the original Sharpe De Michelle et al model.



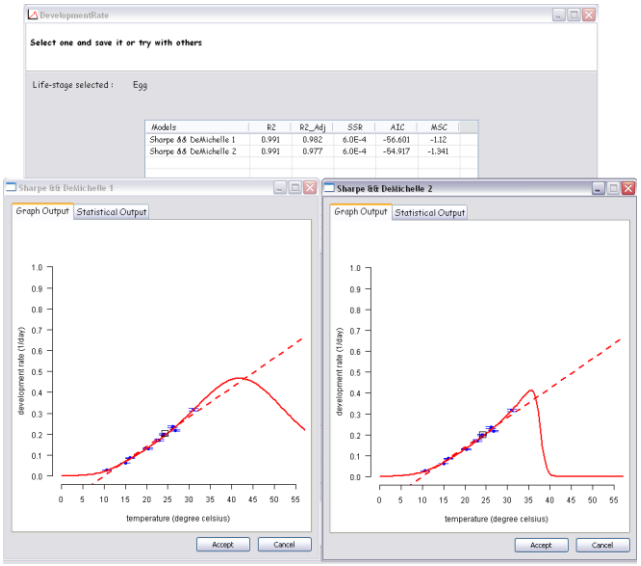
Below is the table that guide ILCYM's users in choosing sub-model

Icon	Description
»	Selecting the entire list of sub-models
›	Selecting a model in the list of sub-models
‹	Removed a model from the list of sub-models
«	Removed all sub-models from the list of sub-models

ILCYM's wizard developmental rate display

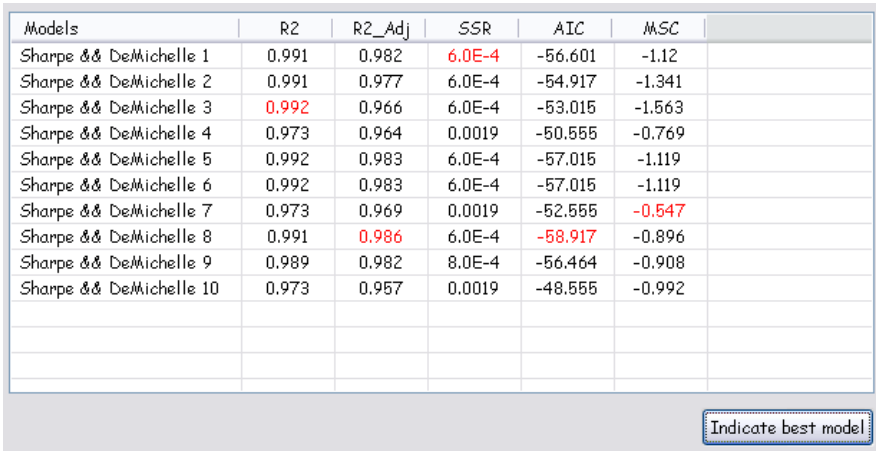


Below is ILCYM's window for two sub-model selections



You can choose all models and compare, is such case several windows will appear with the result in figures and a unique window for parameters estimates comparison.

When you ***click on indicate best model button***, the statistical criteria for selecting best sub-model will appear as below and best model will be mark in **red color**.



Models	R2	R2_Adj	SSR	AIC	MSC
Sharpe && DeMichelle 1	0.991	0.982	6.0E-4	-56.601	-1.12
Sharpe && DeMichelle 2	0.991	0.977	6.0E-4	-54.917	-1.341
Sharpe && DeMichelle 3	0.992	0.966	6.0E-4	-53.015	-1.563
Sharpe && DeMichelle 4	0.973	0.964	0.0019	-50.555	-0.769
Sharpe && DeMichelle 5	0.992	0.983	6.0E-4	-57.015	-1.119
Sharpe && DeMichelle 6	0.992	0.983	6.0E-4	-57.015	-1.119
Sharpe && DeMichelle 7	0.973	0.969	0.0019	-52.555	-0.547
Sharpe && DeMichelle 8	0.991	0.986	6.0E-4	-58.917	-0.896
Sharpe && DeMichelle 9	0.989	0.982	8.0E-4	-56.464	-0.908
Sharpe && DeMichelle 10	0.973	0.957	0.0019	-48.555	-0.992

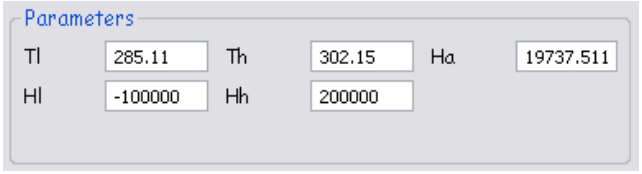
Indicate best model

Single sub-model selection

When this option is selected, you will use a single sub-model at a time; adjust its parameters until a good fitting is obtained.

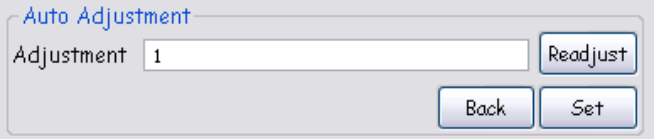
Manually changing sub-model initial parameters (only for single selection)

ILCYM's user can manually change sub-model initial parameters using the window below. You just need to enter your desire value of parameter in the allocated space.



Automatically changing sub-model initial parameters (only for single selection)

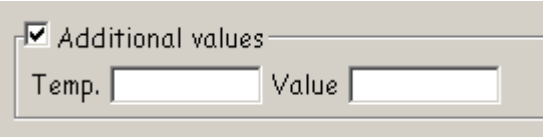
This option is used to automatically modify the initial parameters of a sub-model to ease the convergence of the fitting algorithm. The user adjusts the parameters by clicking on ***Readjust*** *button* to obtain adequate parameter values that can easily converge and provide best fit of the curve. Several clicks on the ***Readjust*** *button* shows changes on the initial curve of the model, when the curve begin converging click on ***Set parameters*** to set the range of initial values of parameters and then click on ***readjust*** until a best initial curve is found. A ***Back button*** is also provided in case you want to return in a passed situation.



Inputting additional values

Sometimes input data does not contain sufficient information that can properly guide the selected sub-model to converge towards threshold temperatures. If the user has any data points on how the species under investigation could behave near-threshold temperature of development, s/he can include these values using the window below. At first you will ***stick the Additional values*** **button,** and then inter a temperature value (lower or high), proceed to the next window to inter the development value.

For example, if you inter two values of temperature (lower and high) you will also enter two values of development corresponding to each temperature. All values should be separated by a comma (,).

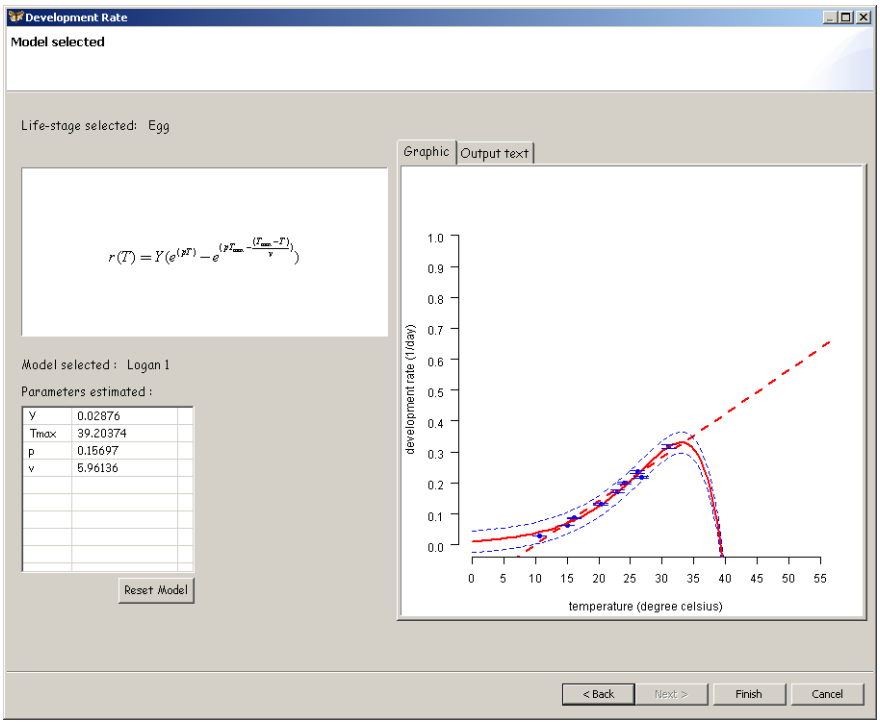


Note: This window for additional values can also be used to input additional data points that were not intitally include in the input data. Always remember that for each temparature corresponds a value of developmental rate and all

are separated by a comma(,) . **Example: Temp.** 10, 12, 15, 25, 36 **Value** 0.1, 0.2, 0.4, 0.8, 0.1; in this example you have 5 temparatures, which stipulate that 5 values of development rate are needed.

Reset model button allows resetting the model selected. To select new model just ***click on the life-stage button*** and ***choose another model***.

Below is ILCYM's display of a single sub-model selection.



On the right side of the window, a graph is displayed with the observed data point (i.e. the median development rates and the 95% CL determined from the previous analysis); experimental data points are provided in blue, and the resulting curve using these parameters is shown in the graph (red line).

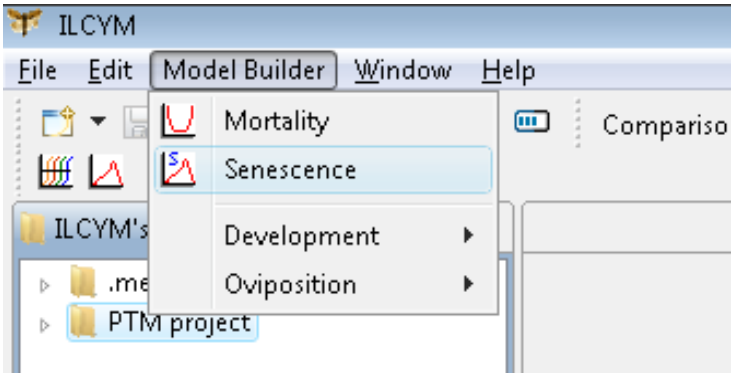
Note: To ensure that your choosing model was correctly saved in the worspace of the program, you must press next , next,…, and the ***finish button*** a window will appear displying the selected model, his parameters and the graph.

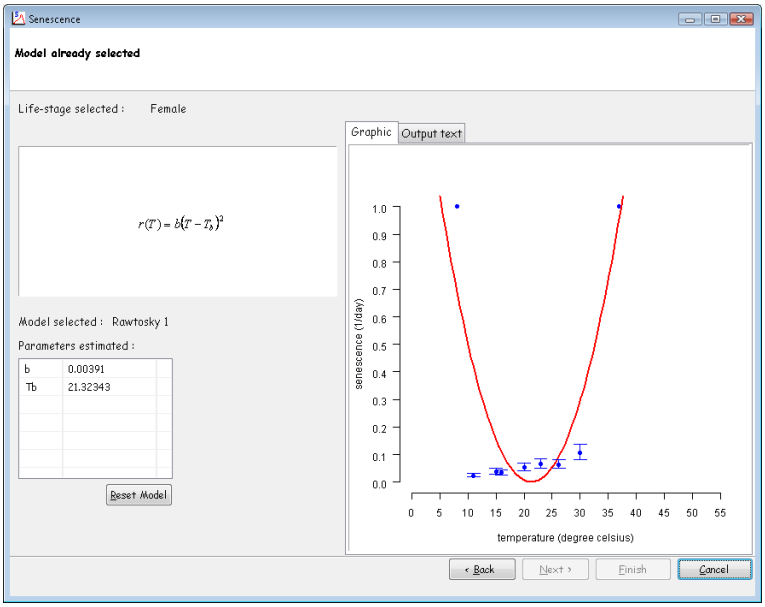
Changing scale on the graph

To change the **scales** (axis) or input **title** you need to right ***click on the model window*** (window which only contains your chosen model) and go to "**Properties**", then write the number or text in the "**Scale Area**".

c) Senescence

At adult stages ("males" and "female"), because the insects die instead of developing to a next stage, the sub-model in this section describes the temperature-dependent senescence rate. ILCYM software provides a number of sub-models just as for development rate that can be used for describing temperature-dependent senescence rate. The process of model selection is identical as on develomental rate.

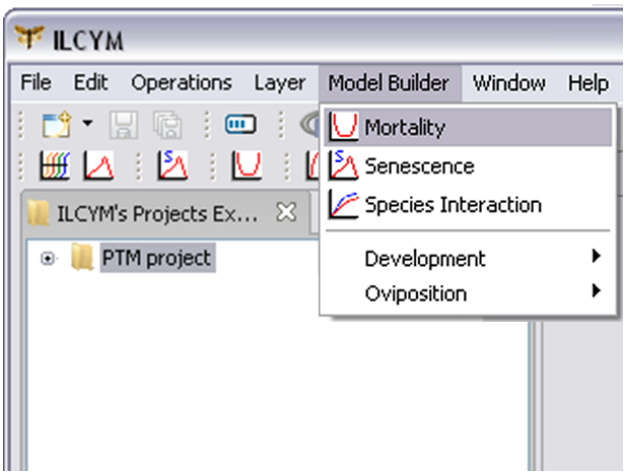




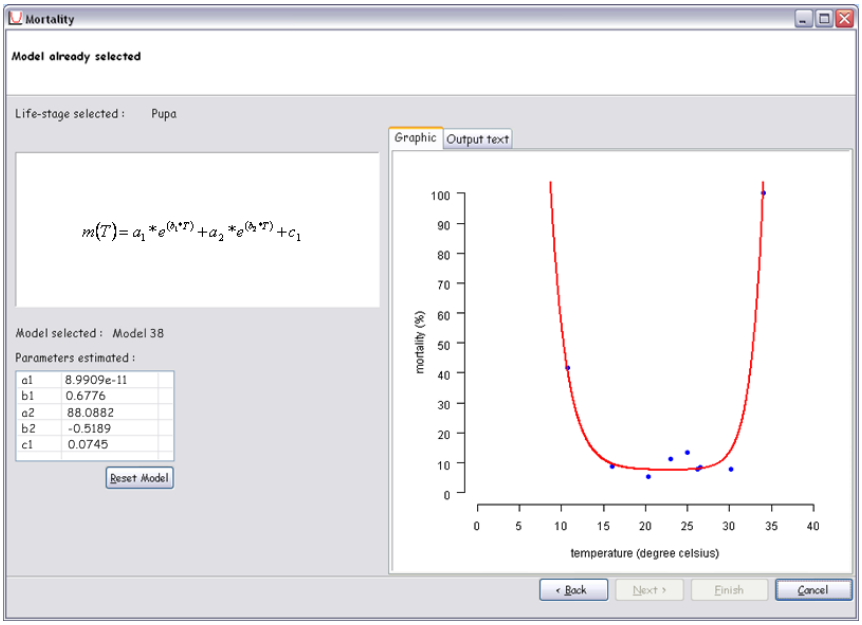
d) Mortality

Mortality is another important process in an insect life cycle that is affected by temperature. ILCYM's quantify the effect of temperature on the immature stages (egg, larva, and pupa) of the insect life-cycle. Many non-lineal models that can best describe the mortality induced by temperature (low mortality near an optimal temperature and mortality increase with the deviation from the optimal temperature) are given in this program.

The best sub-model can be selected based on the available statistic just like in the previous life stages.



Here you can modify the functions and their respective initial parameters depending on how they fit to the data. Adjusting the parameters as described in the section "*Modifying initial parameters.*



The above window displays the results of an evaluation of mortality. The left side of the screen shows the statistics of the analysis and on the right side a graph displays model results.

At optimum temperature for development, the mortality is lowest but increases at high and low temperature depending on the insect species.

The statistical analysis shows the estimation of the parameters of the best model used to quantify the effect of the temperature on the mortality.

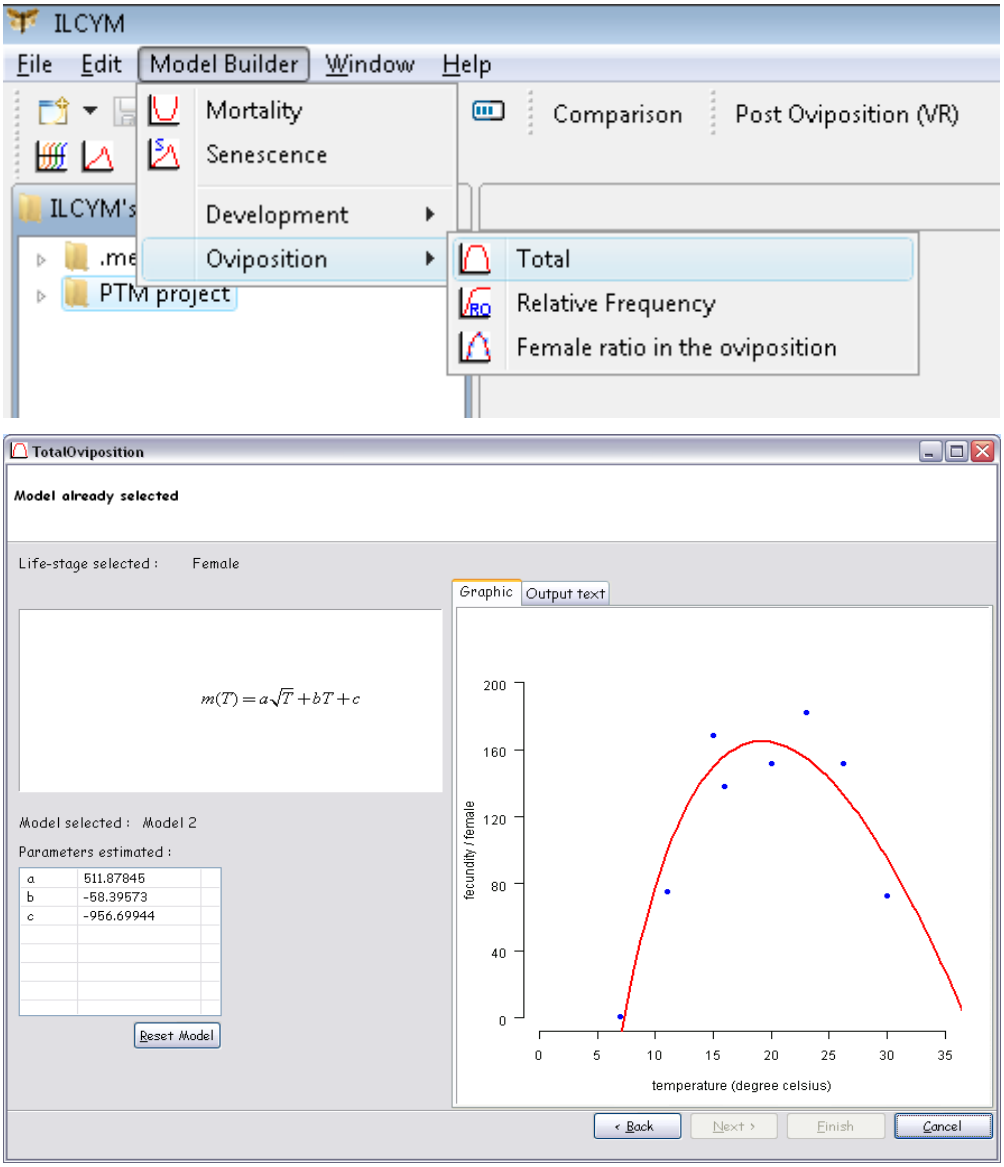
e) Reproduction

The oviposition or reproduction of insects can be described by three temperature dependent components: the total oviposition, the relative oviposition frequency and the age-specific survival rate, (each of this component are directly linked to the option initially chosen by the user during the creation of a new project, see page 35).

i) Total oviposition

In ILCYM, total oviposition represents the expected total number of eggs laid per an insect female during her whole life span as a function of temperature.

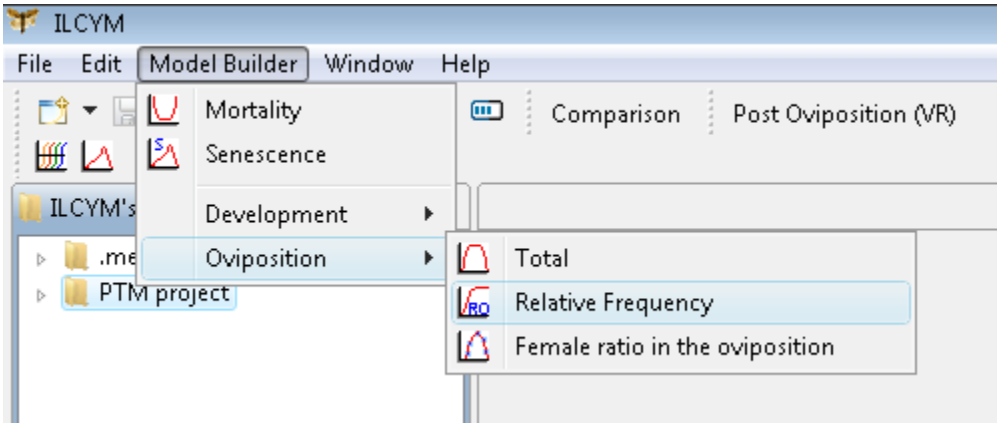
This relationship is modeled with a nonlinear function as shown in the graph below.

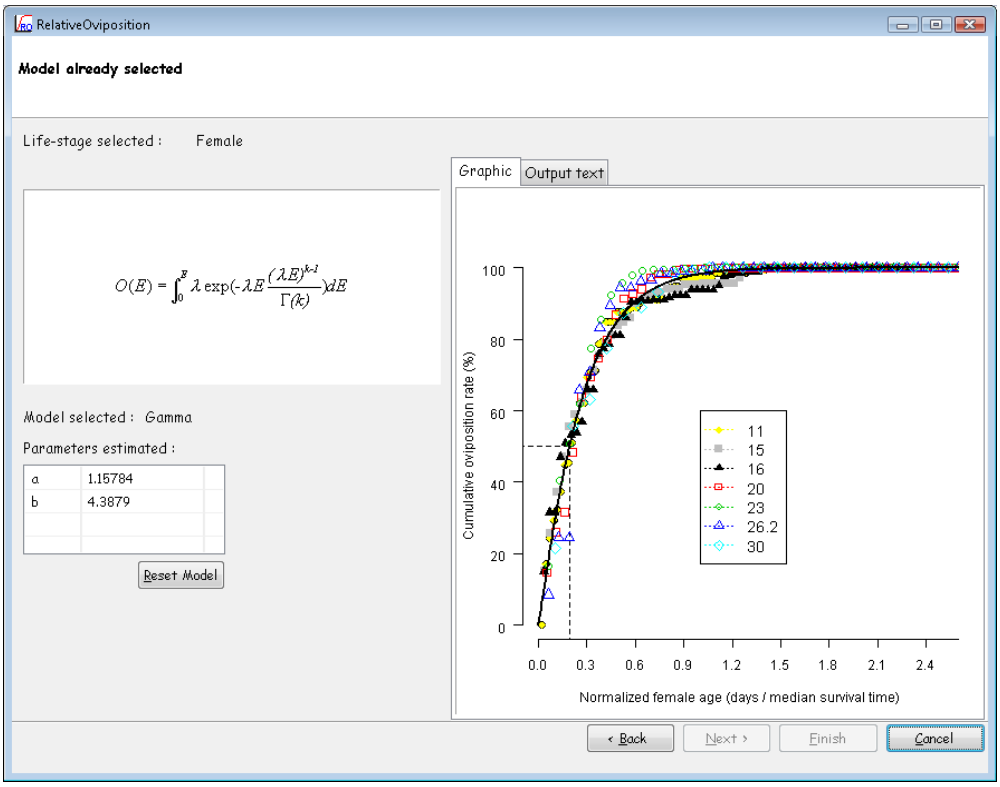


ii) Relative oviposition frequency

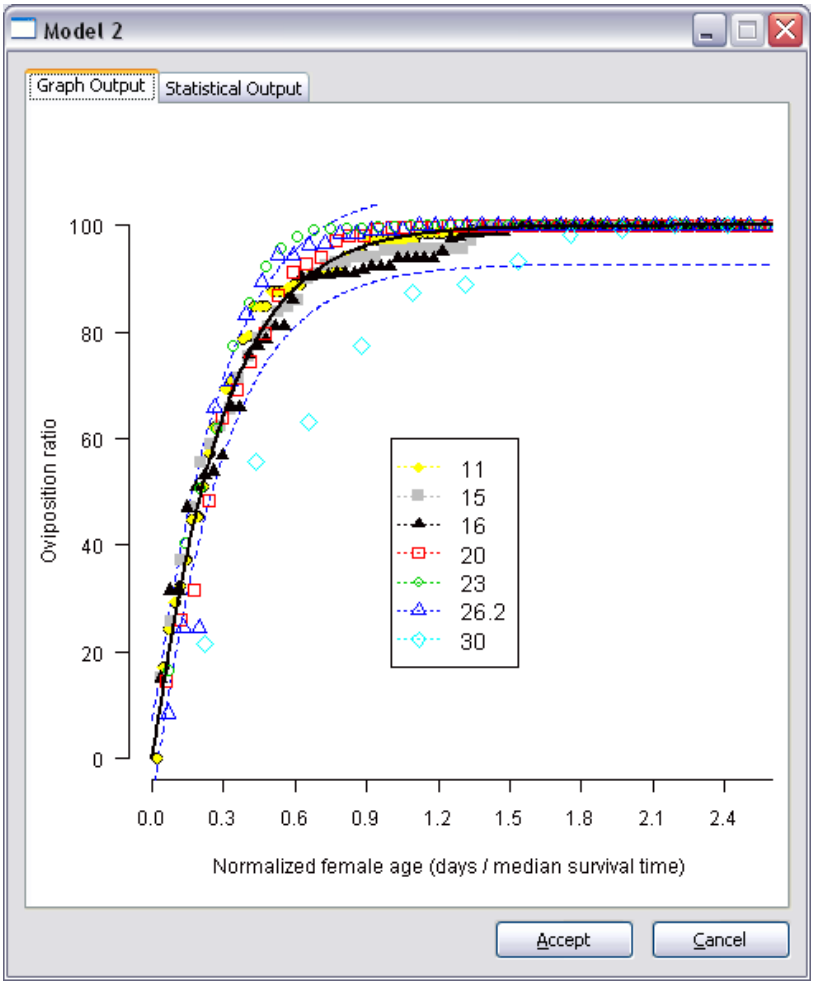
The relative oviposition frequency is the proportion of total lifetime reproductive potential that elapses during each time period. This accumulated oviposition frequency of the females is evaluated in relation to the normalized age of the females (time/median time) at a determined temperature.

The statistical analysis shows the estimation of the parameters of the best model used to quantify the effect of the temperature on the total oviposition of the females per day.





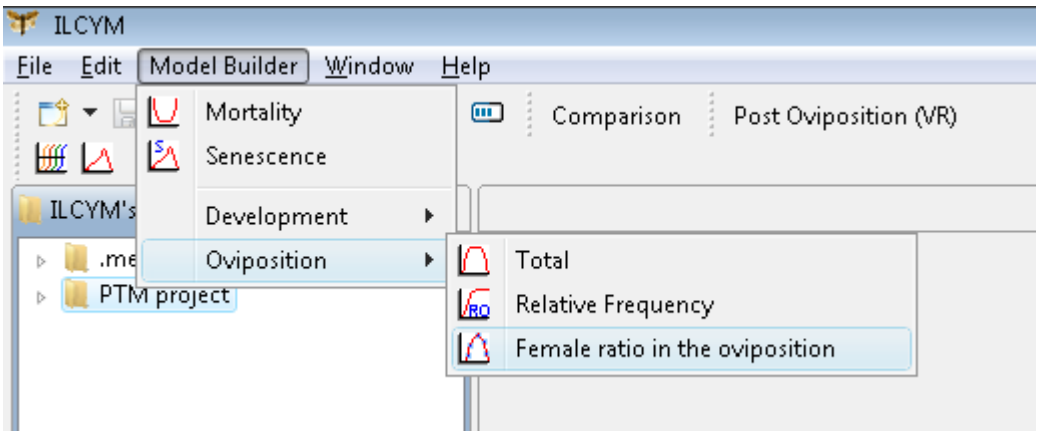
Note: While conducting this analysis, it will be preferable to choose only one model at time, no multiple models selection is recommended here.

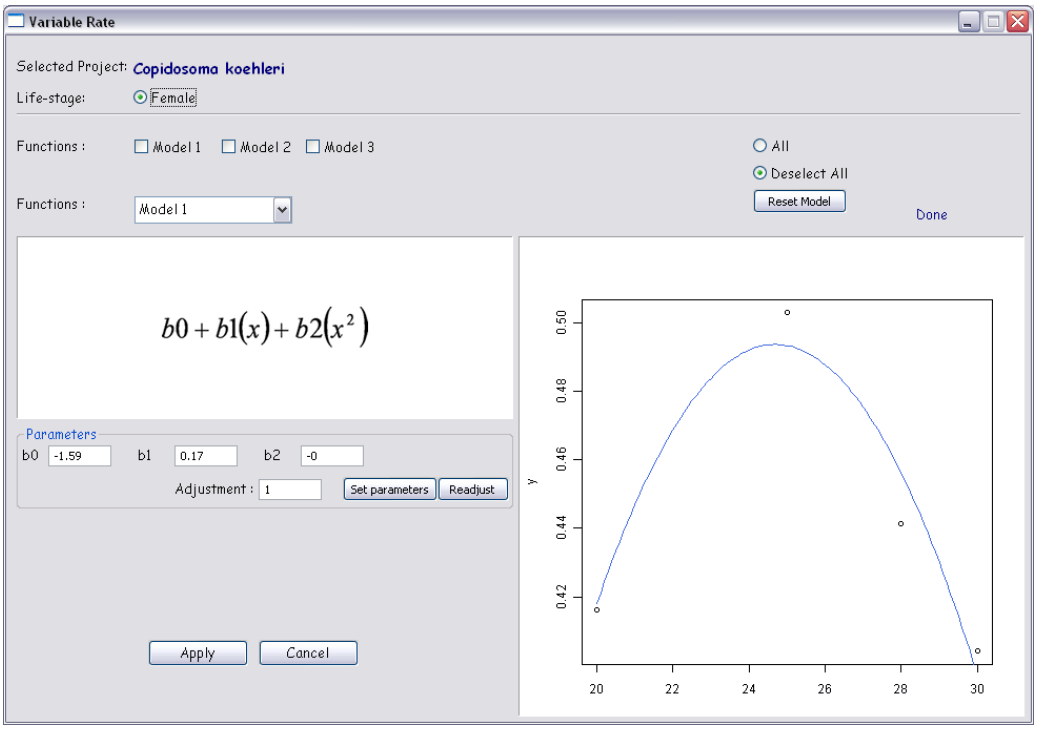


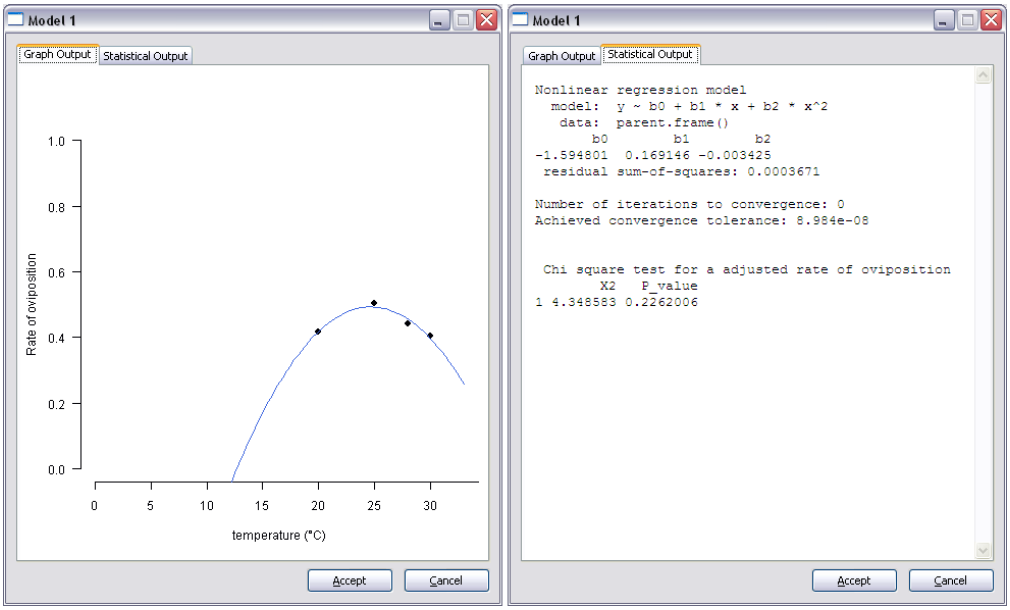
iii) Variable rate of oviposition

It believed that insect fecundity may be limited by temperature in different levels; either during period of eggs maturation or through the time requisite for strategic ovipositing of the eggs. Hence insect females cannot foresee the number of oviposition opportunity that she may encountered on a given day, the optimal rate of egg maturation may therefore depend on the trade-off associated with egg and time limited oviposition. Owing to the fact that females of different size may as well have different amount of body reserves, size-dependent allocation trade-offs between the females' condition and their eggs production may be expected.

ILCYM's allows the user to fit a nonlinear function describing oviposition frequency of female as show on the following windows.







iv) Female ration in the oviposition

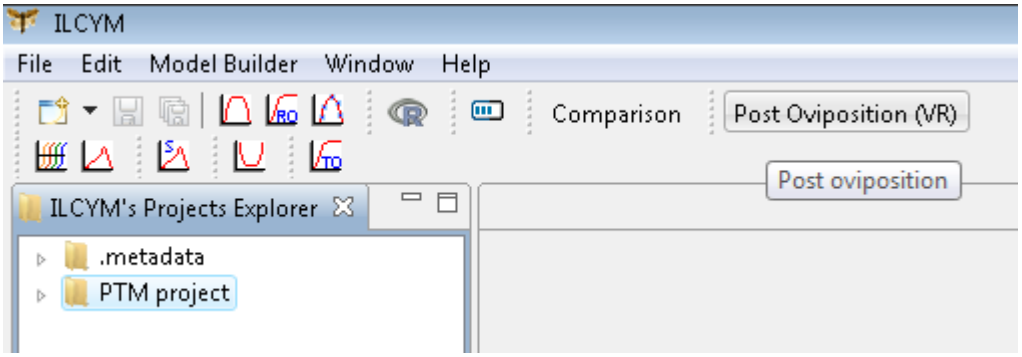
For incomplete life table where two oviposition files (for male and female oviposition respectively) are loaded as input data, a function representing female ration in the oviposition is selected through fitting and added into the overall phenology model.

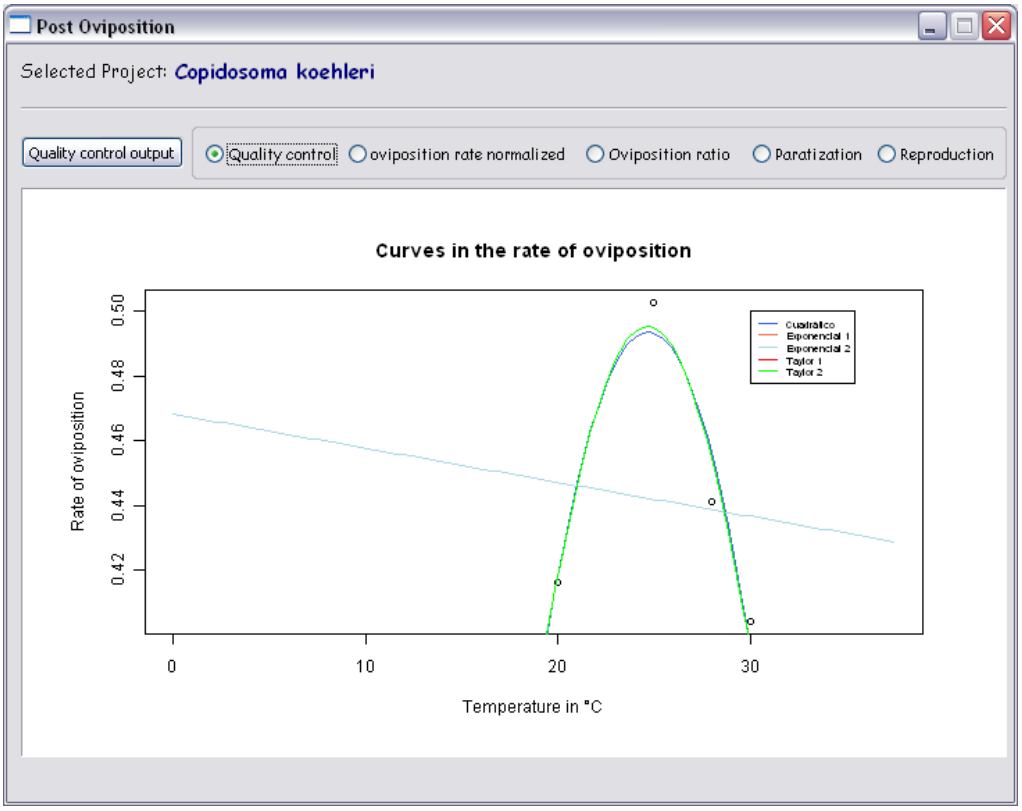
Note: The variable oviposition rate analysis is only includes on the overall phenology for species with variable rate usually defined when creating a project.

v) Complement analysis: Post Oviposition (VR)

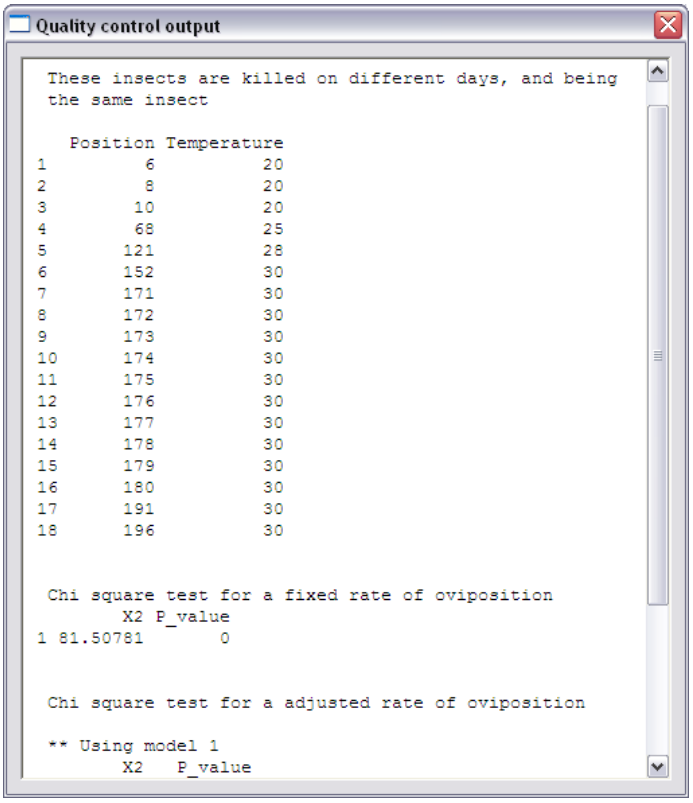
The post oviposition in ILCYM stands for age-specific survival rate that described the proportion of number of eggs alive at any given age (time).

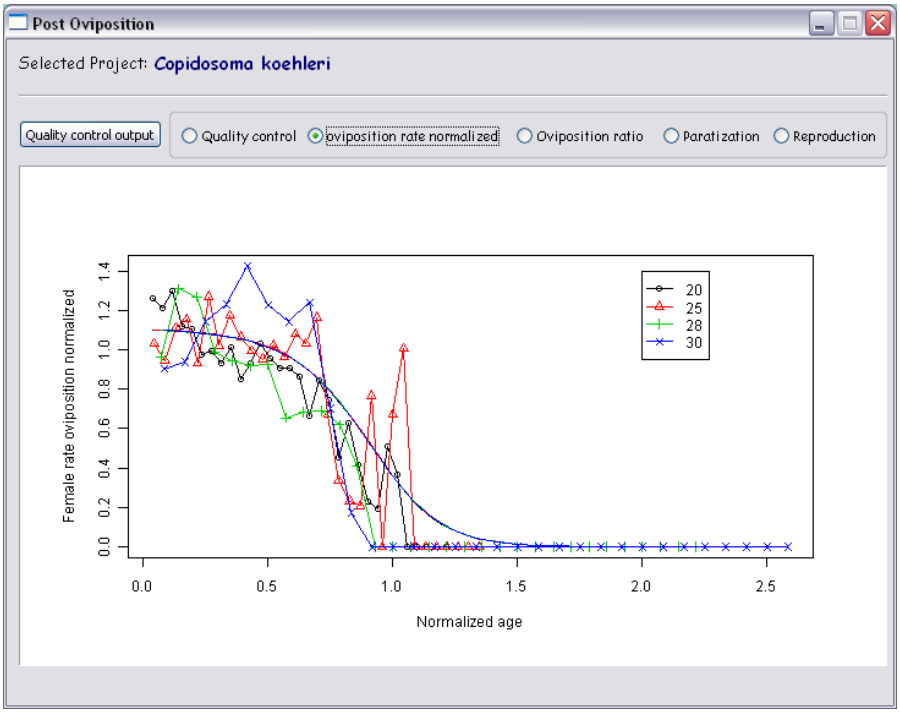
This evaluation is only made when the oviposition rate is variable; that means when the female oviposition rate depends on age or temperature.


ILCYM
File
Edit
Model Builder
Window
Help
Comparison
Post Oviposition (VR)
Post oviposition
ILCYM's Projects Explorer
.metadata
PTM project

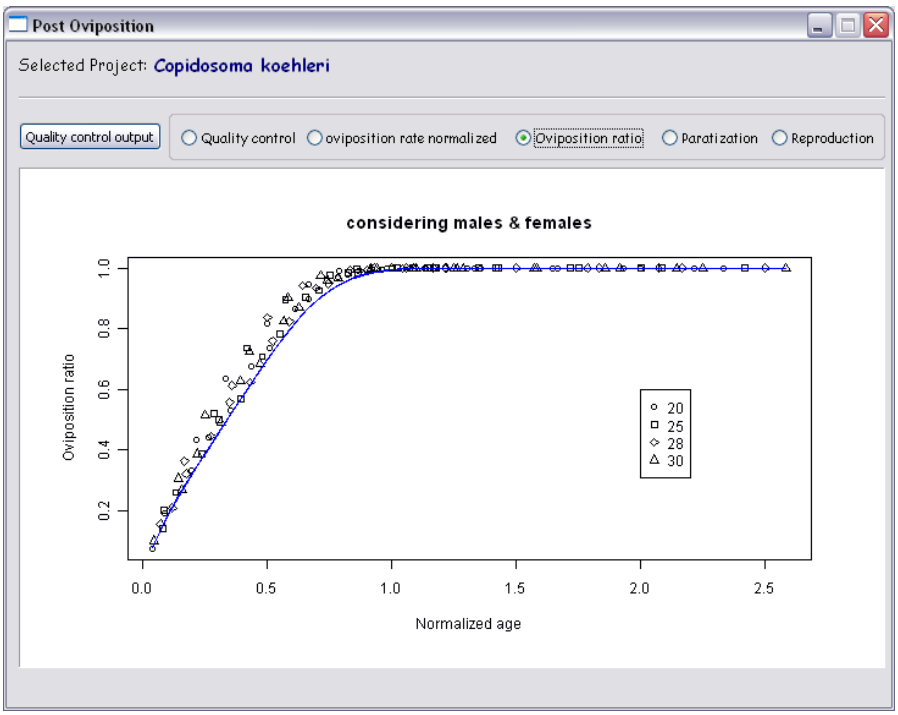

Post Oviposition
Selected Project: Copidosoma koehleri
Quality control output
Quality control
oviposition rate normalized
Oviposition ratio
Paratization
Reproduction
Curves in the rate of oviposition
Rate of oviposition
0.42
0.44
0.46
0.48
0.50
0
10
20
30
Temperature in °C
Cuadratico
Exponencial 1
Exponencial 2
Taylor 1
Taylor 2

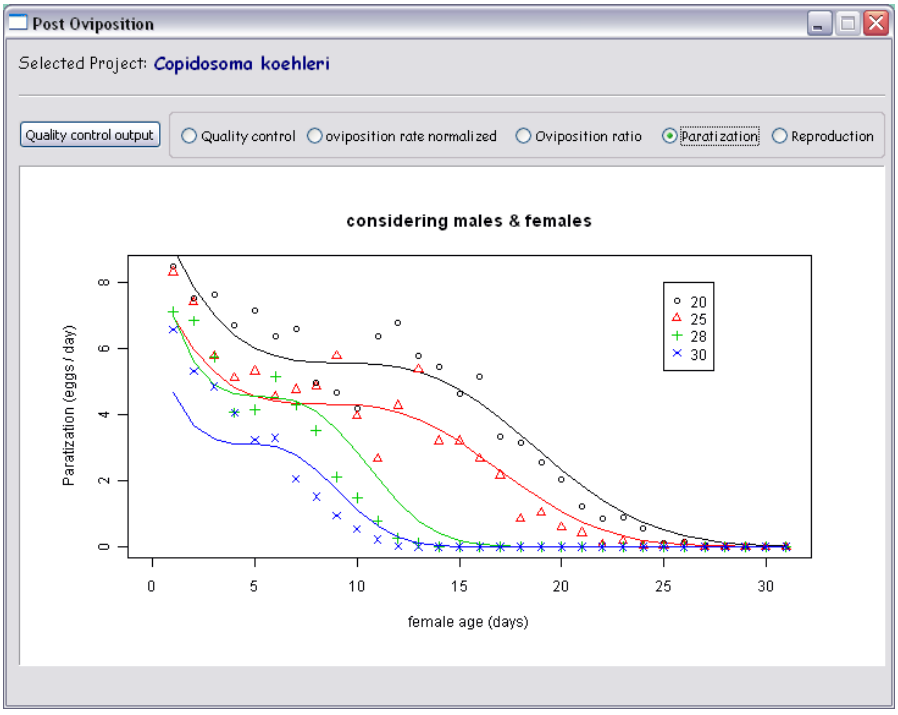
By **clicking** on ***Quality control output button*** the user can view the statistical quality control output.

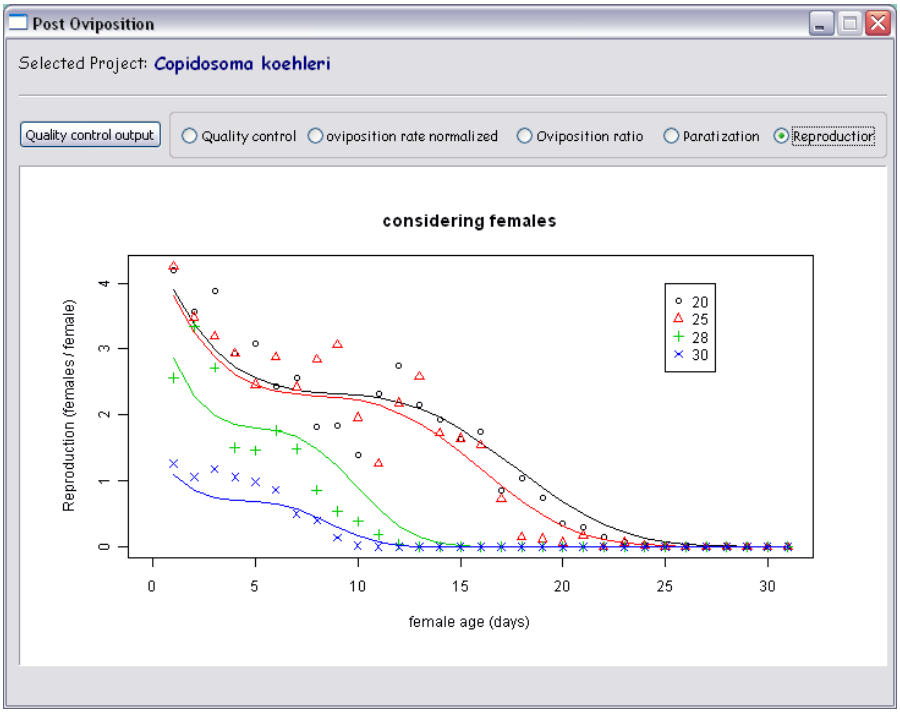




This is a nonlinear model used to describe the relationship between the cumulative proportions of *P. operculella* eggs and parasitized per female and normalized female age.





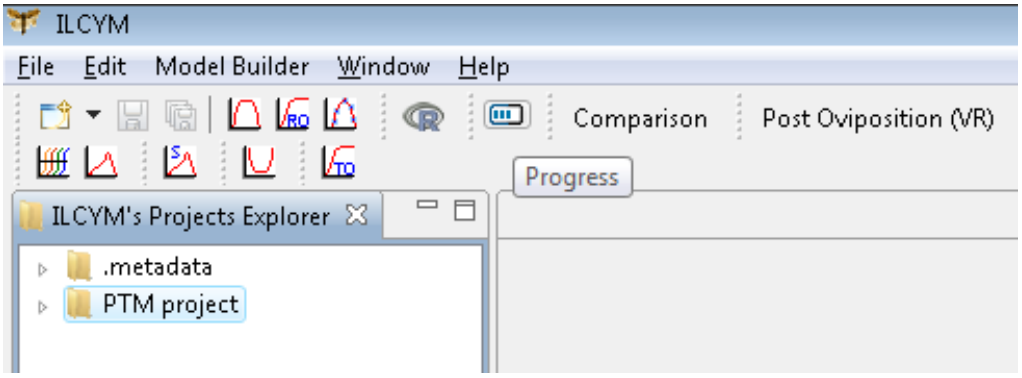


Markers: observed data (means); ***solid lines*:** fitted models.

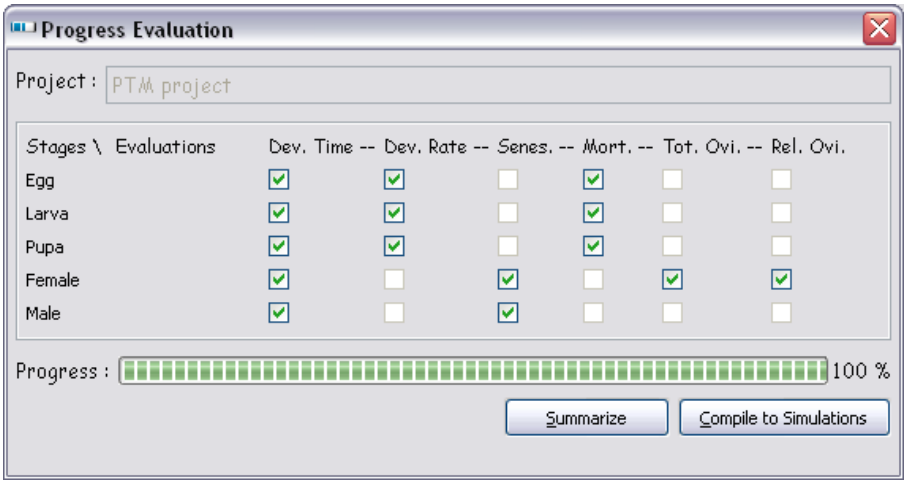
Note: ILCYM only provide a visual display of post oviposition analysis. These outputs are not included on the overall phenology of the species under investigation.

3.1.7 Project progress

To know about the progress of your project, ILCYM has a tool that show at each moment the stage of the progress in developing a phenology this tool can be found in ***Progress menu***

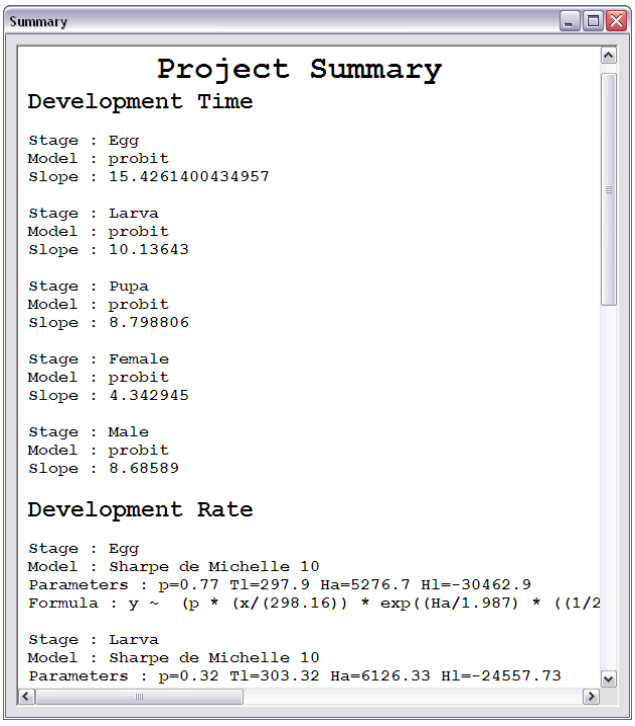


The screen below shows the insect developmental stages that have been evaluated; the stages evaluated are check (the ones that have not been marked) are the ones that cannot be evaluated under the conditions the experiments have been made.



3.1.8 Project summarize

Click on ***Summarize*** **button** the window below will appear and display a project resume, with the summary of each life-stage and its parameters and functions selected in "**Model Builder**" during the development of your project.

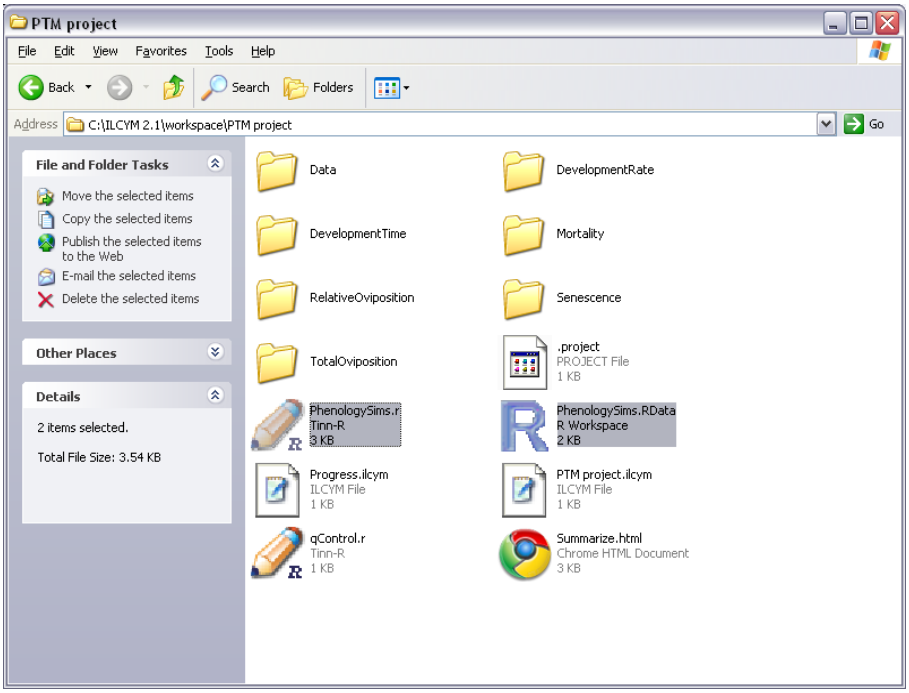


Note: It required once you complete the development of a complete phenology model for a your species, click on summary to cross check that all life stages of your insect were well saved and are included in the summary file. Additionally verify that the name, number and the mathematical expression of the equation that you have accepted when ***clicking on finish bottom***, is identical to what was saved for each life stage. If these details are not made you may not be able to proceed to model validation and simulations

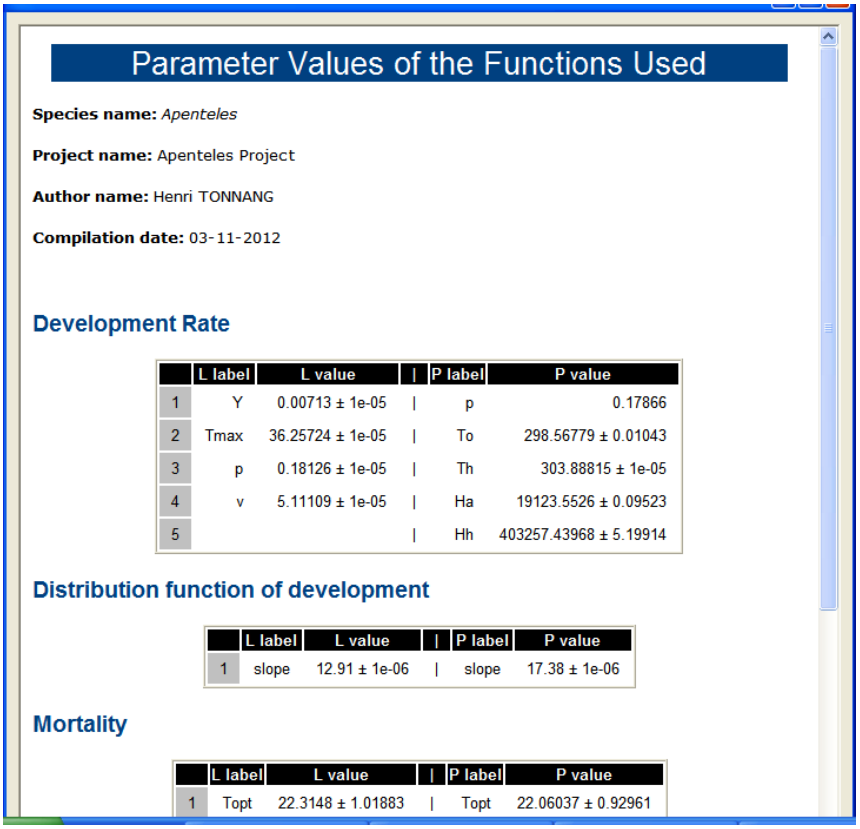
3.1.9 Compiling project

Click on ***Compile simulation*** **button**, the project will be compiled; all functions and parameters will be organized in a special format to be read in R and used for simulations.

This process takes few seconds and when it is finished the progress windows will disappears and 2 files will be created, ***PhenologySims.Rdata*** and ***PhenologySims.r*** inside the project folder in workspace. These files will be used for subsequent analysis in ILCYM.



Below is another file that automatically appears when your phenology model is completely developed. The file displays the all parameters and functions selected for the overall phenology model.



Parameter Values of the Functions Used

Species name: *Apenteles*

Project name: Apenteles Project

Author name: Henri TONNANG

Compilation date: 03-11-2012

Development Rate

	L label	L value	|	P label	P value
1	Y	0.00713 ± 1e-05	|	p	0.17866
2	Tmax	36.25724 ± 1e-05	|	To	298.56779 ± 0.01043
3	p	0.18126 ± 1e-05	|	Th	303.88815 ± 1e-05
4	v	5.11109 ± 1e-05	|	Ha	19123.5526 ± 0.09523
5			|	Hh	403257.43968 ± 5.19914

Distribution function of development

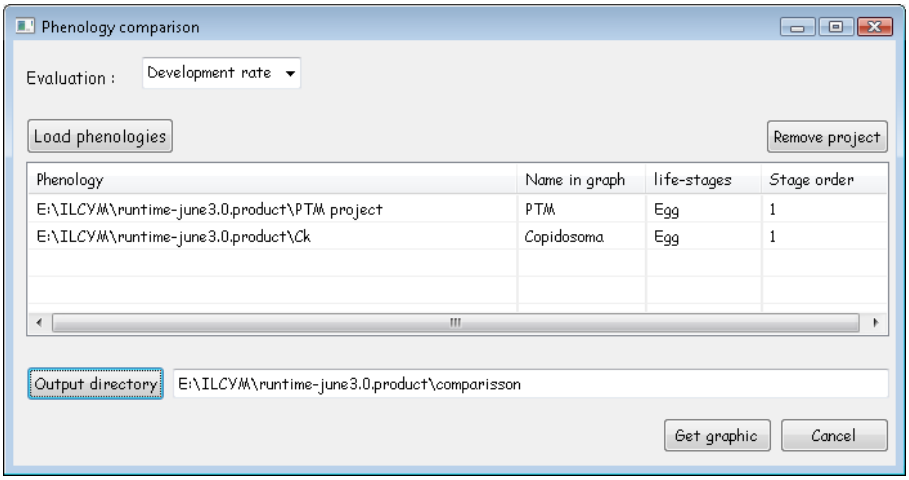
	L label	L value	|	P label	P value
1	slope	12.91 ± 1e-06	|	slope	17.38 ± 1e-06

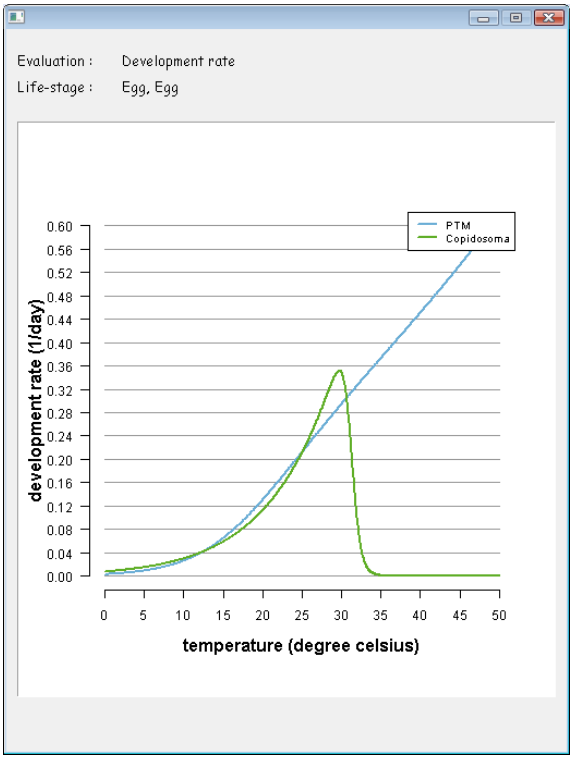
Mortality

	L label	L value	|	P label	P value
1	Topt	22.3148 ± 1.01883	|	Topt	22.06037 ± 0.92961

3.1.10 Project comparison

This feature allows users to compare same stages of different insect species. On model builder window ***clik comparison***, the window below will appear, select the stage you want to compare and load their completed phenolonogy model succesively and click on get graph to visualize the overlapping outputs.

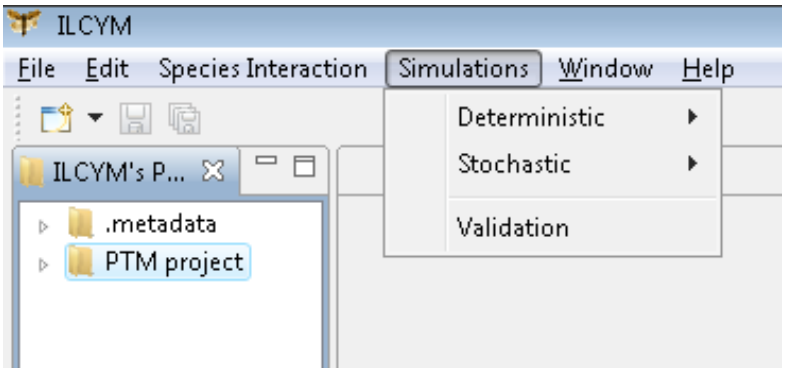




Note: The comparison can only be operated on the same life stage and ILCYM allows a maximum of three species to be compared at the same time. It is also preferable to compared species with identical number of immature life stages in their aver phenology model.

3.2 Validation and Simulations

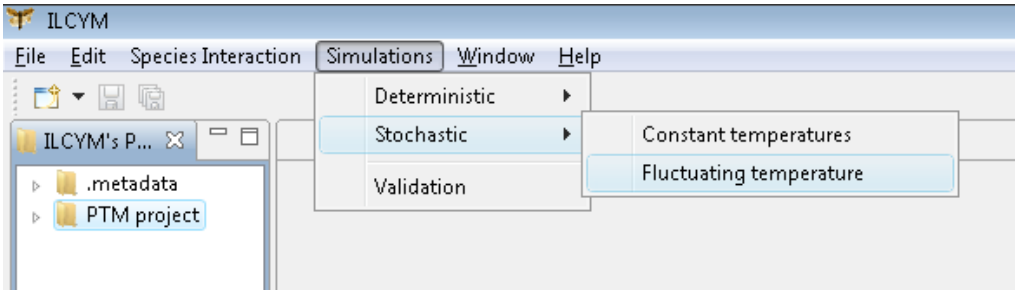
ILCYM users can conduct two (2) type of simulations: stochastic and deterministic. For each simulation the life table parameters of your species are estimated. The simulations are found in the ***Simulations Menu*** below.



3.2.1 Stochastic Simulation

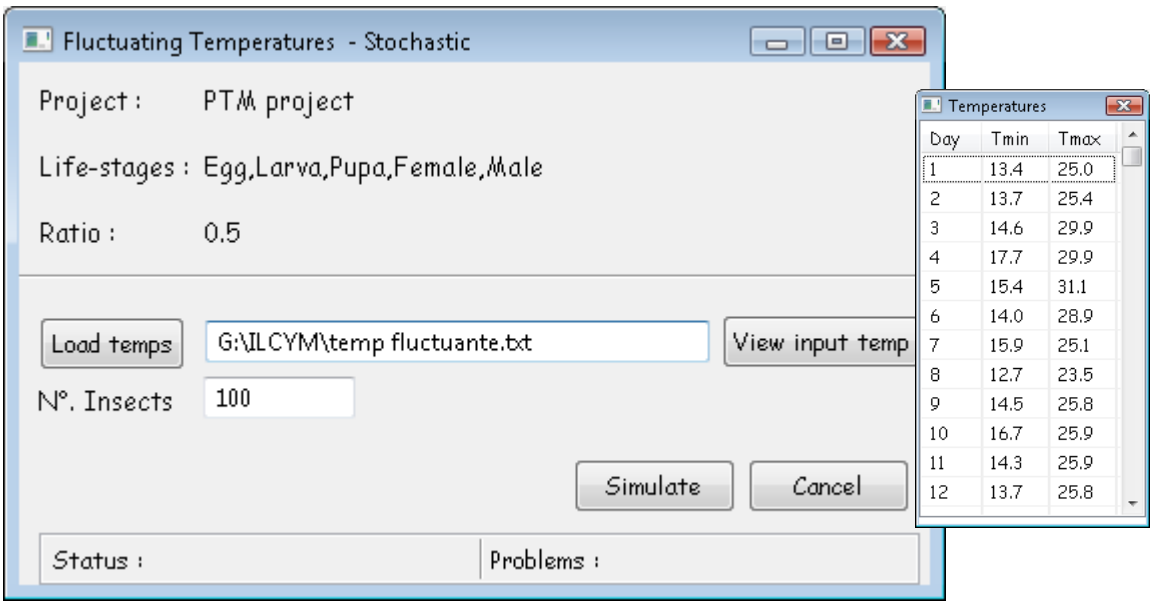
ILCYM stochastically simulates a user-defined number of life tables, each with a user-defined number of individuals, through rate summation and random determination for each individual's survival, development to the next stage, and sex under constant or fluctuating temparature. Stochasticity in reproduction is calculated according to the variance observed in the data on total oviposition per female used for developing the model.

a) Stochastic Simulation at fluctuating temperature



The following window will appear. The menu has two sub-menus.

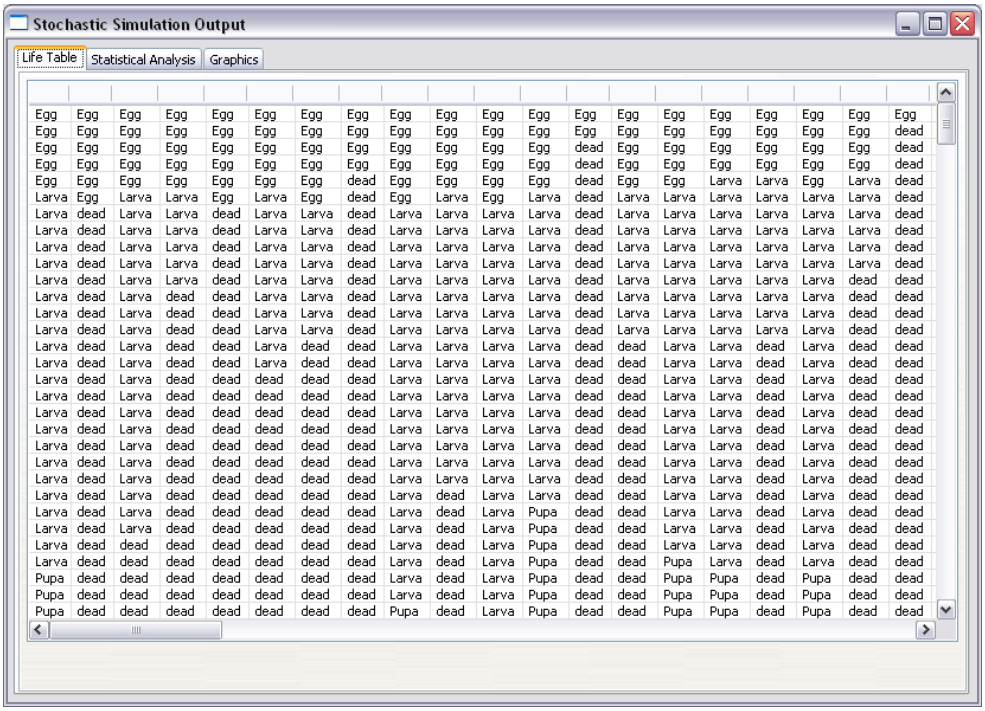
Click on ***simulation button*** for life-stage simulation.



- ***Project:*** PTM project (user most selected the project once on the simulation window)
- ***Life-stages:*** Egg, Larva, Pupa, Female, Male (here you have all the life stages of your species as defined during project creation)
- ***Ratio***, ratio between males and females (this parameter was defined during project creation).
- ***Load temps:*** this button allows the user to load temperature data
- ***N^0. Insect:*** number of insect to be simulated.
- ***View input temp:*** This button allows user to view their input temperature
- ***Simulate button*****:** start the simulation process
- ***Cancel button:*** help user to cancel the operation.

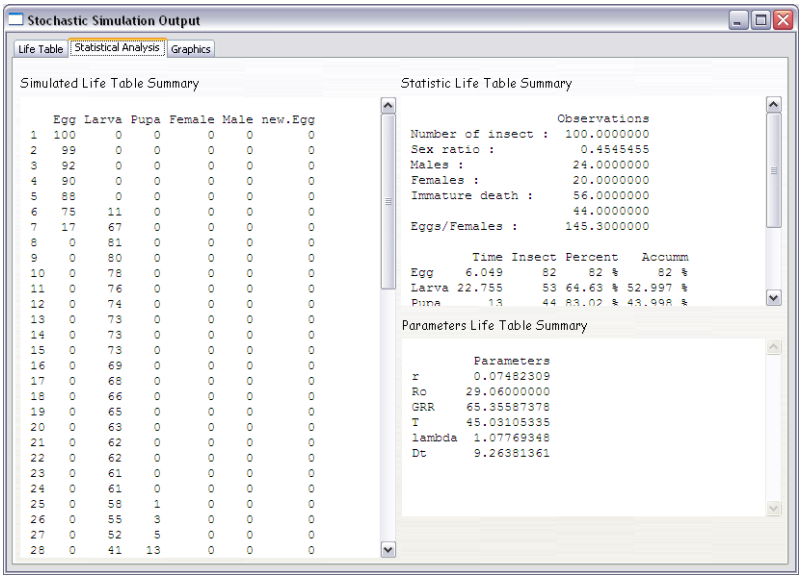
i) Output life-table

Once you click on the ***simulation button*** the application will simulate a life-table with all the data for your selected phenology and the temperature that was inputted in the previous step.



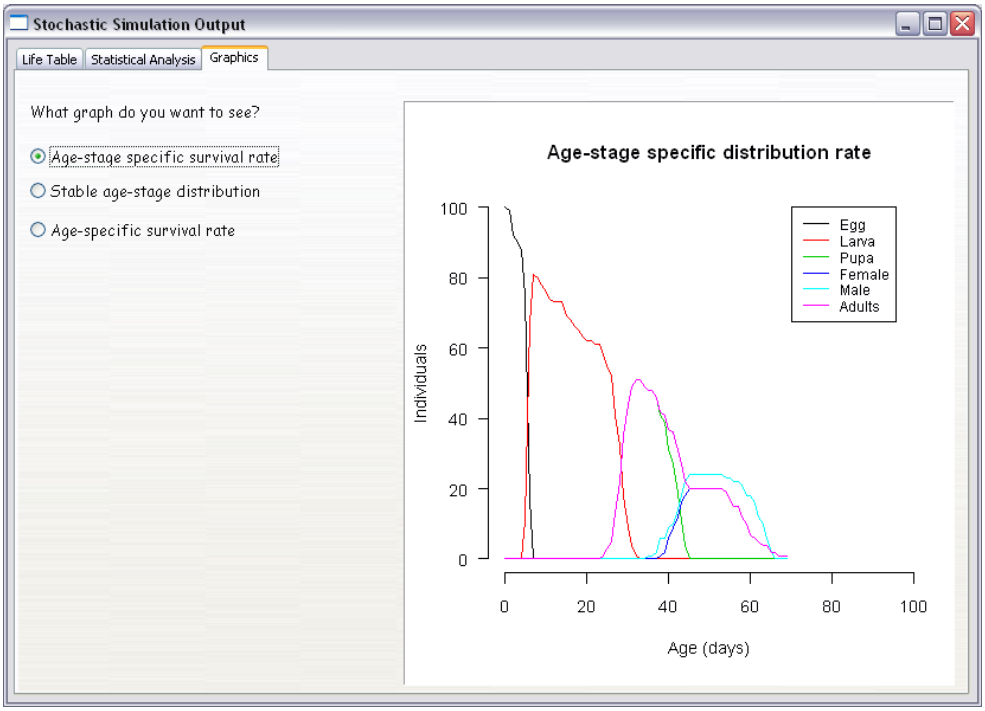
ii) Statistical summary

The screen below shows the summary of the simulated life-table (on the left) and related life-table statistics (e.g., sex ratio, fecundity, development time, etc.) and calculated life-table parameters (e.g., r_m, intrinsic rate of natural increase; R_0, net reproduction rate) (on the right).

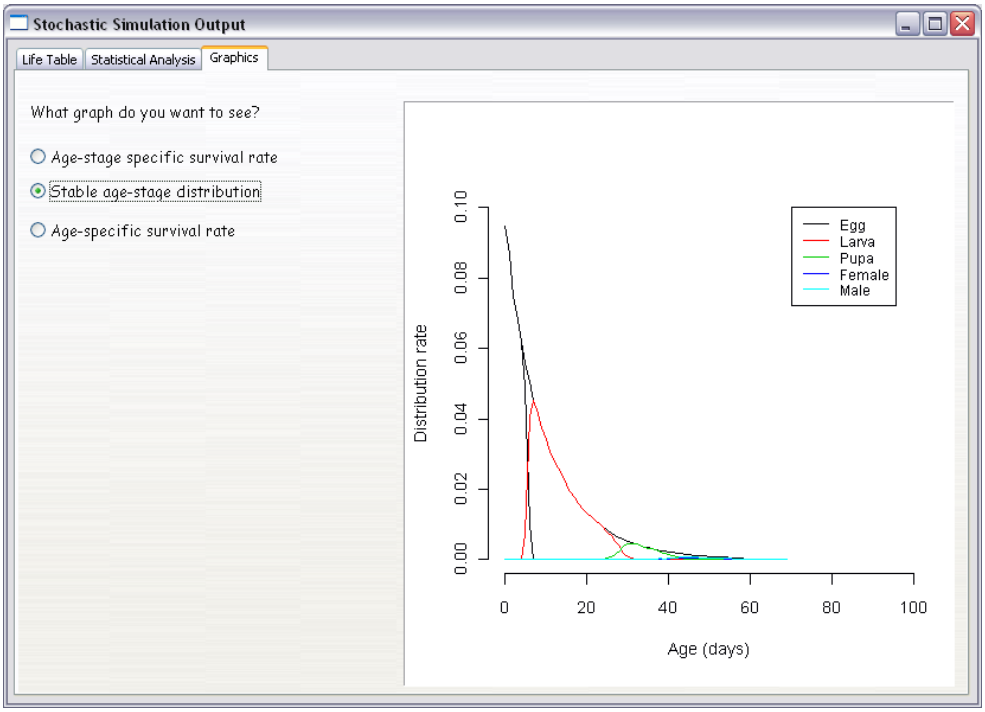


iii) Graphics

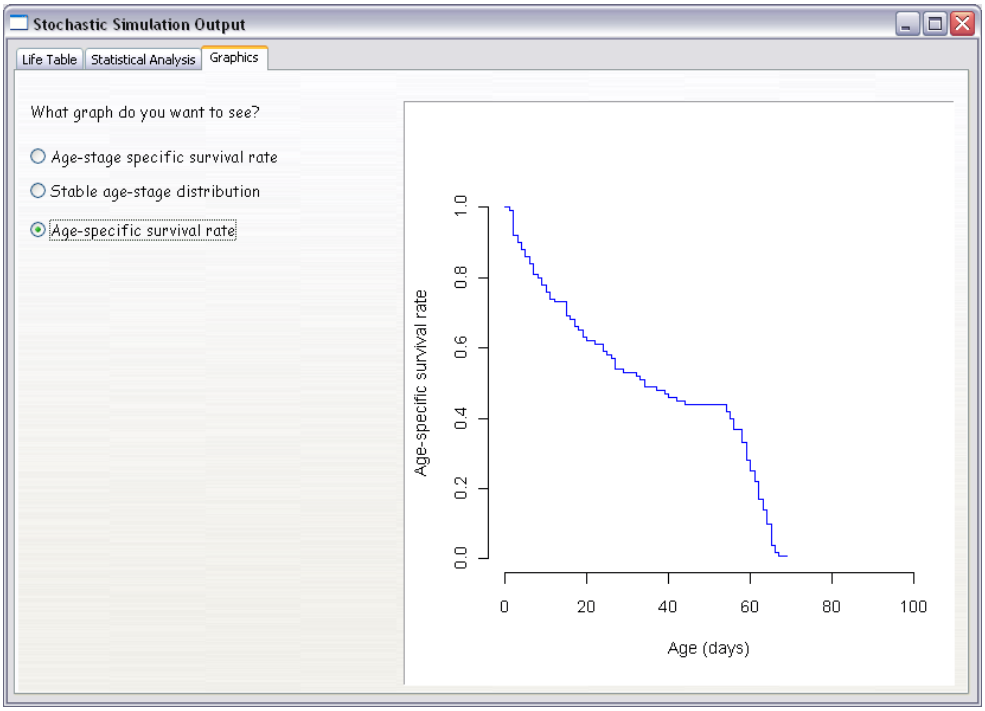
Age-stage specific distribution rate



iv) Age-stage distribution

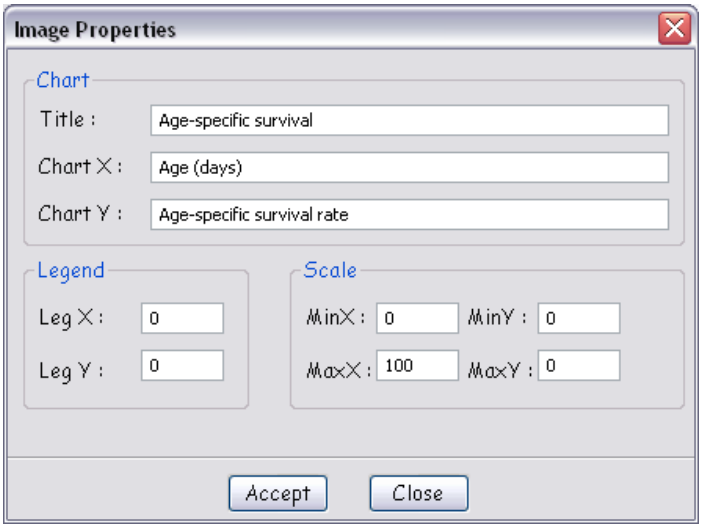


v) Age-specific survival rate



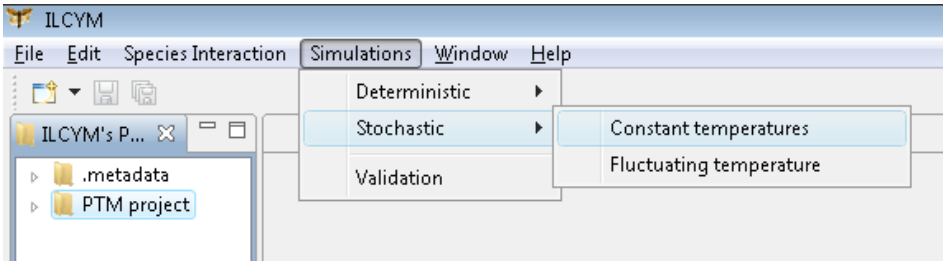
vi) Modifying the scale of the graphs

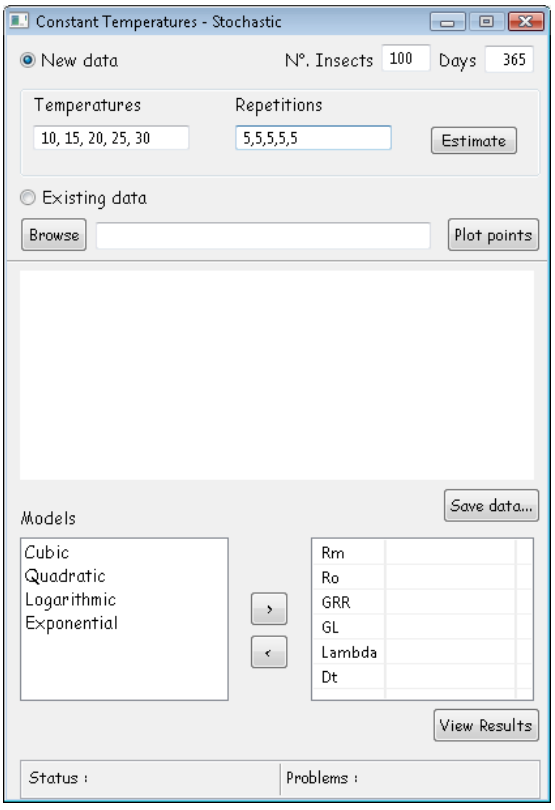
In some cases the graph does not show the plot correctly, to see it well, ***right click*** on the graph and select ***Properties***. Modify the scales, legend or chart and ***click on Accept button.***



b) Stochastic simulation at constant temperatures

This tool allows the simulations under constant temparatures.



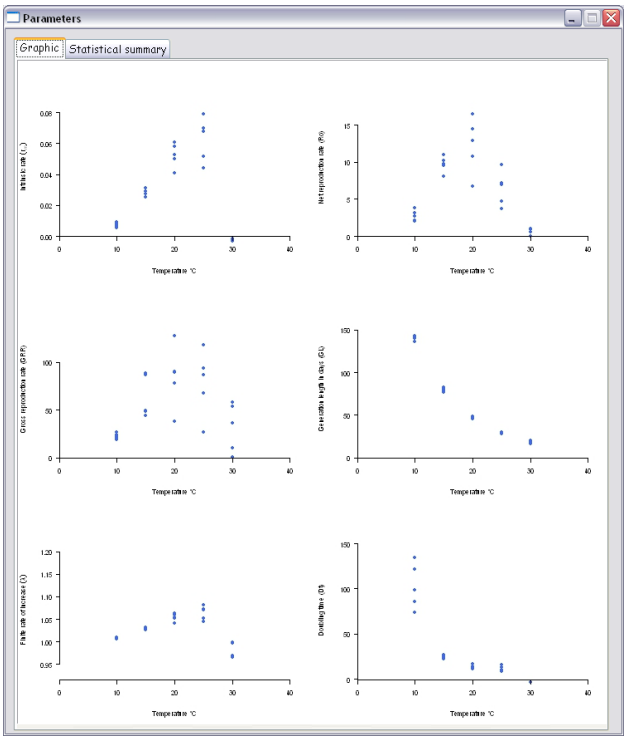


- ***New data*:** select for simulating life table parameters at constant temperatures then fit the points with curve.
- ***N^0. Insect:*** number of insect to be simulated.
- ***Days:*** number of days for the simulation, usually 365 representing one year.

- ***Temperatures* text box:** here the user must enter the temperatures separated by comma (,), for each temperatures corresponds a number of repetitions.
- ***Repetitions* text box:** for inputting the number of repetitions separated by comma (,)
- ***Estimate* button:** this button runs the simulation.
- ***Existing data* option:** select this option to conduct simulation with existing data.
- ***Browse* button:** use this button to check for data simulated.
- ***Plot points* button:** for plotting data points recently simulated or the data loaded.
- ***Models* list:** list different type of model for fitting life table parameters simulated points.
- ***Save button:*** save the data
- ***View results button:*** display the results.

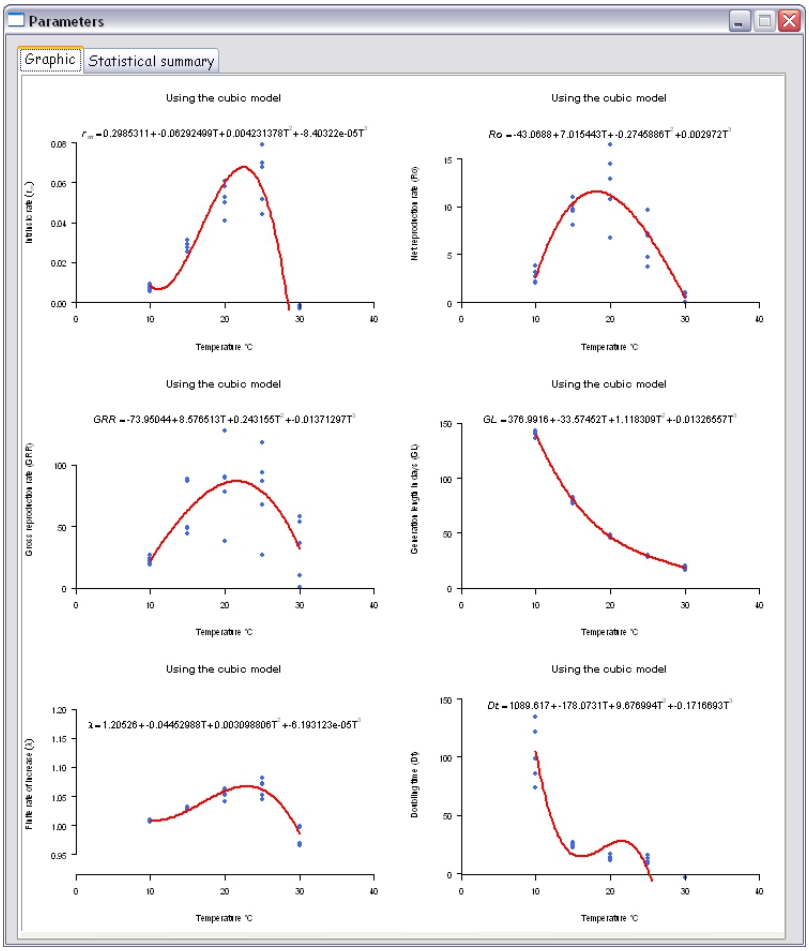
i) Displaying life table parameters

The window below will appears when you click on plot point's button.



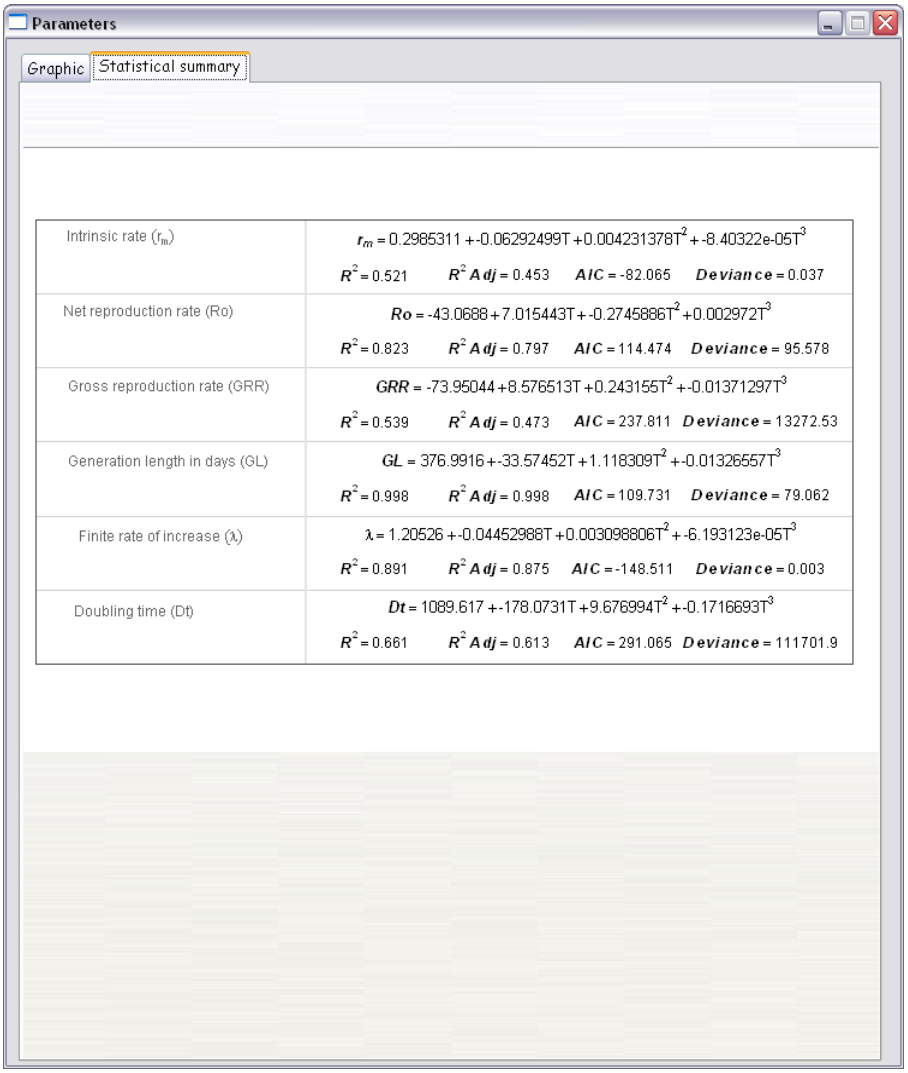
ii) Fitting life table parameters to non linear functions

The following window appears when the user selects the model to fit the life-table parameters. ILCYM has inbuilt nonlinear functions that can be used to fit the life table parameters. The best-fitted function can be compared to the output results from deterministic simulation for the same species. In doing that ILCYM's users can confirm the performance of the simulation algorithms implemented in the software. It is expected that the best fitting curve from stochastic simulation should be similar to the curve yielded by the deterministic simulation.

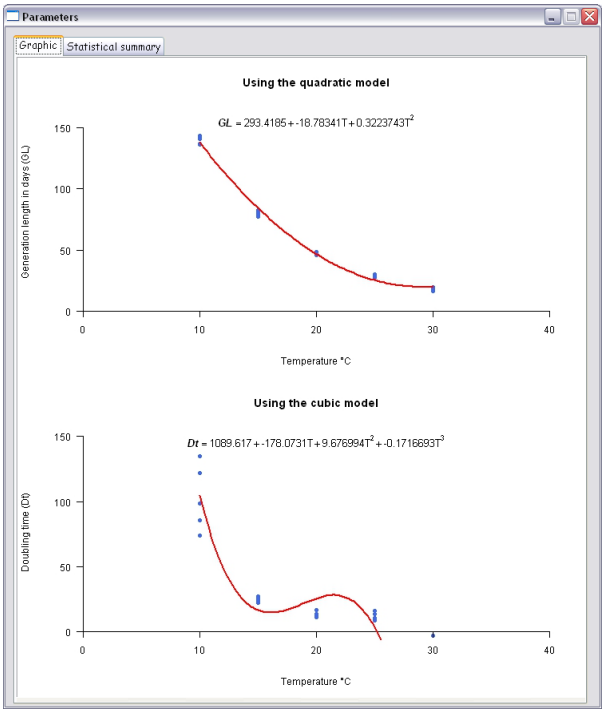


iii) Summary life table parameter and statistical outputs

This windows display the parameter name and the models equations.



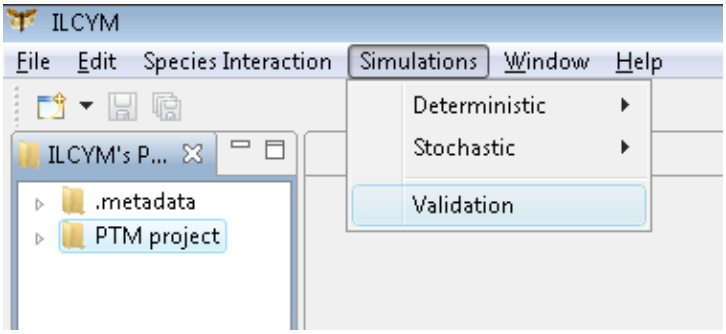
There is the possibility for the user to fit parameter of his/her choice with any model.

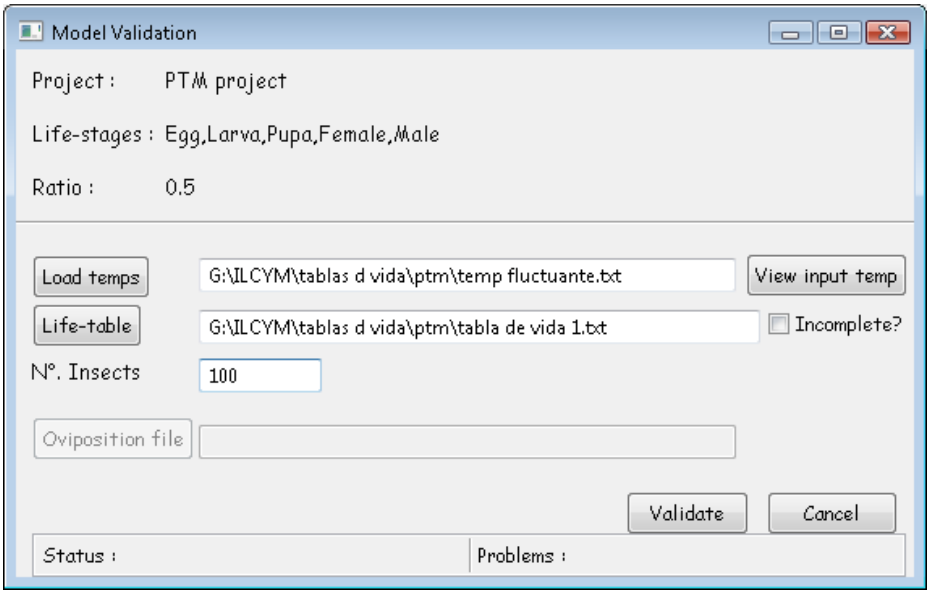


3.2.2 Model validation (validation of established model is done using stochastic simulation)

The validation tool in ILCYM allows the user to evaluate the ability of the developed phenology model to reproduce the insect species behavior under fluctuating temperature conditions.

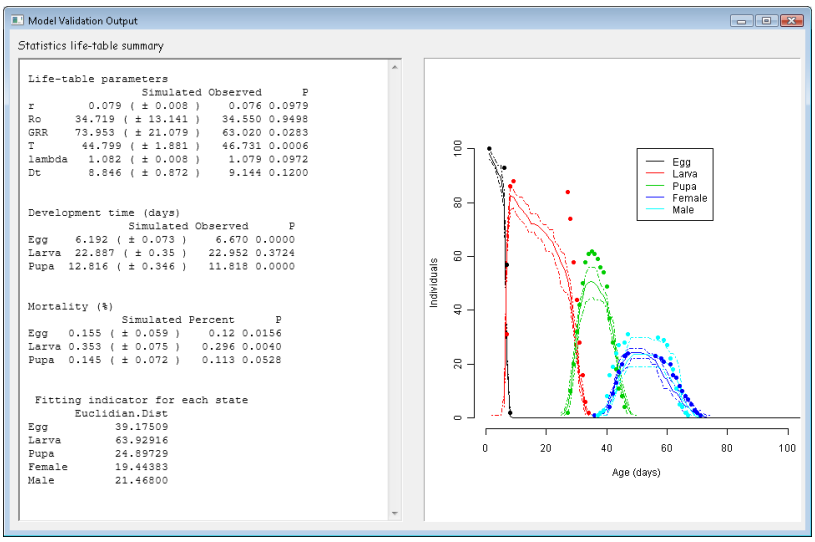
This is achieved by comparing experimental life table data obtained from fluctuating temperature studies with model outputs produced by using the same temperature records as input data.





- ***Life-table* button:** for inputting life-table files used to validate your develop model with fluctuating temperature.
- ***N^0 insects*:** number of insects used for the simulation
- ***Load temps* button:** this button allows loading the data; this data must be in daily format.
- ***Validate* button:** start the validation process.
- ***Cancel* button:** close model validation window.

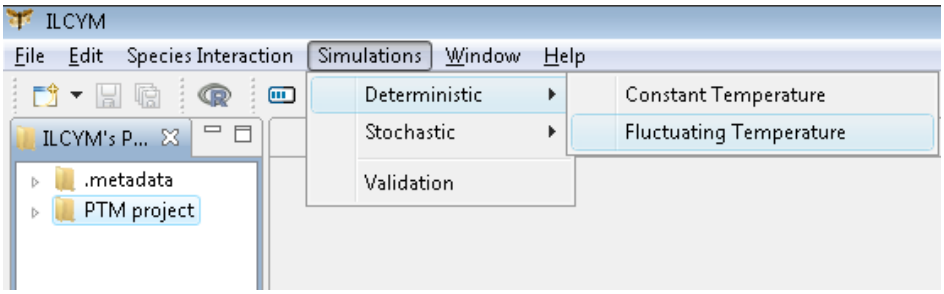
i) Output graph for model validation


Model Validation Output
Statistics life-table summary
Life-table parameters
Simulated Observed P
r 0.079 (± 0.008) 0.076 0.0979
Ro 34.719 (± 13.141) 34.550 0.9498
GRR 73.953 (± 21.079) 63.020 0.0283
T 44.799 (± 1.881) 46.731 0.0006
lambda 1.082 (± 0.008) 1.079 0.0972
Dt 8.846 (± 0.872) 9.144 0.1200
Development time (days)
Simulated Observed P
Egg 6.192 (± 0.073) 6.670 0.0000
Larva 22.887 (± 0.35) 22.952 0.3724
Pupa 12.816 (± 0.346) 11.818 0.0000
Mortality (%)
Simulated Percent P
Egg 0.155 (± 0.059) 0.12 0.0156
Larva 0.353 (± 0.075) 0.296 0.0040
Pupa 0.145 (± 0.072) 0.113 0.0528
Fitting indicator for each state
Euclidian.Dist
Egg 39.17509
Larva 63.92916
Pupa 24.89729
Female 19.44383
Male 21.46800
Egg
Larva
Pupa
Female
Male
Individuals
Age (days)

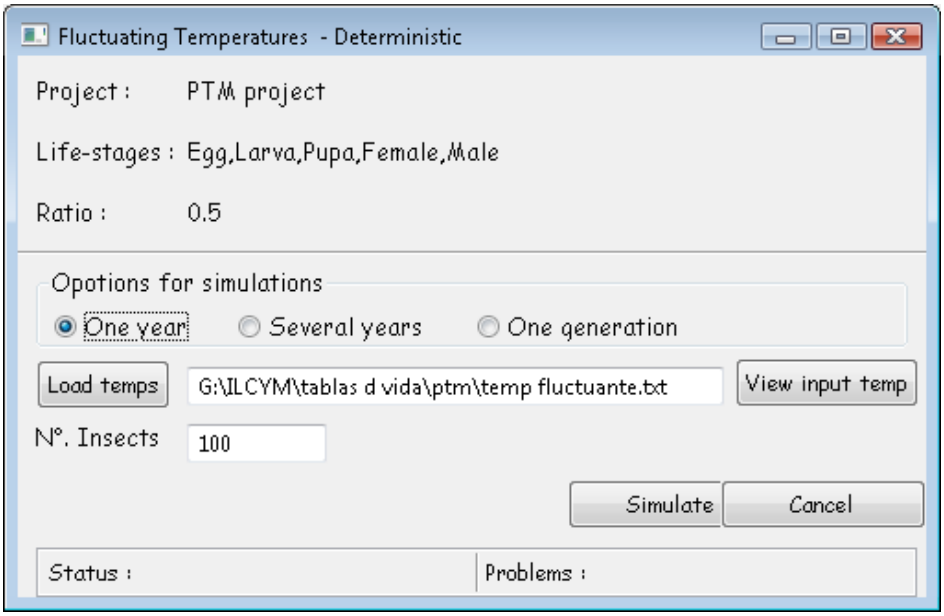
The ***dots*** are experimental results and the ***lines*** are phenology model outputs.

3.2.3 Deterministic simulation

The deterministic simulation simulates population using a rate summation and cohort up-dating approach throughout a long-term period (one or more years) with multiple overlapping generations for a specific location based on minimum and maximum daily temperatures and visually output the potential population increase. At the present stage of ILCYM development, this simulation considers only the growth process as an unbounded process in which the population grows without limit if uncontrolled. Such simulation can be conducted under constant or fluctuating temperature within a period of a generation, one year and several years.



This window will appear.

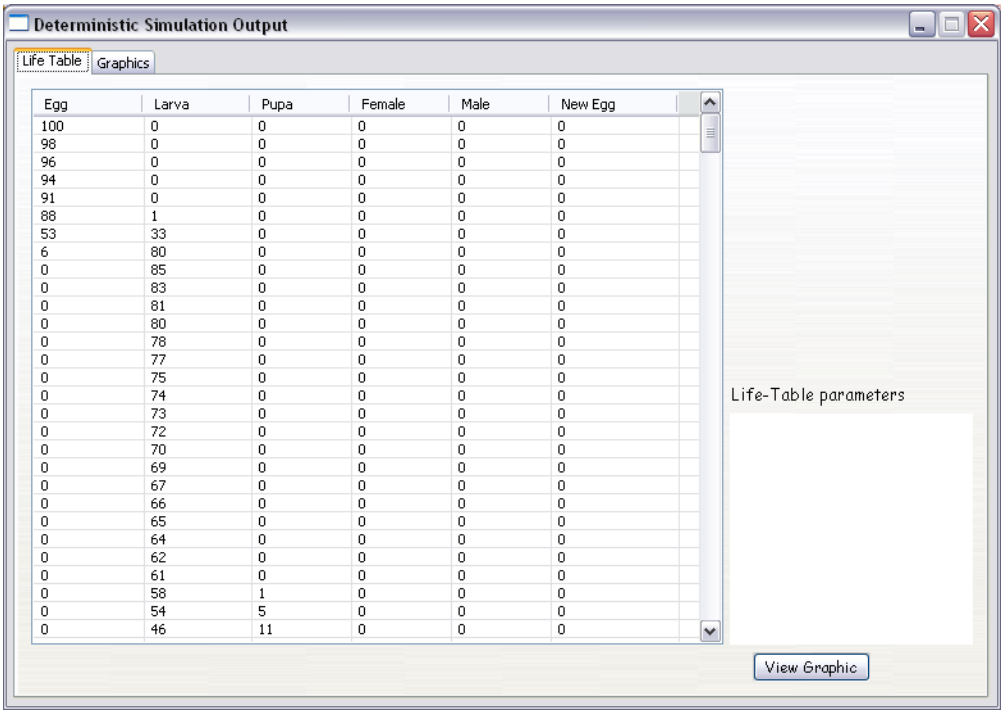


- ***One year option:*** simulates a life-table for one year.
- ***Several years'* option:** simulates life-tables for the subsequent years.

- ***One generation* option:** simulates a life-table for one generation, the life-table parameters are calculated with this option.
- ***N^0 insects*:** number of insects used for the simulation
- ***Load temps* button:** allows the user to load its own temperature data
- ***Simulate* button:** simulates the life-table.
- ***View input temp.*** For viewing the input temperature for the simulation
- ***Cancel* button:** closes the window of deterministic simulation.

i) Displaying life table parameters

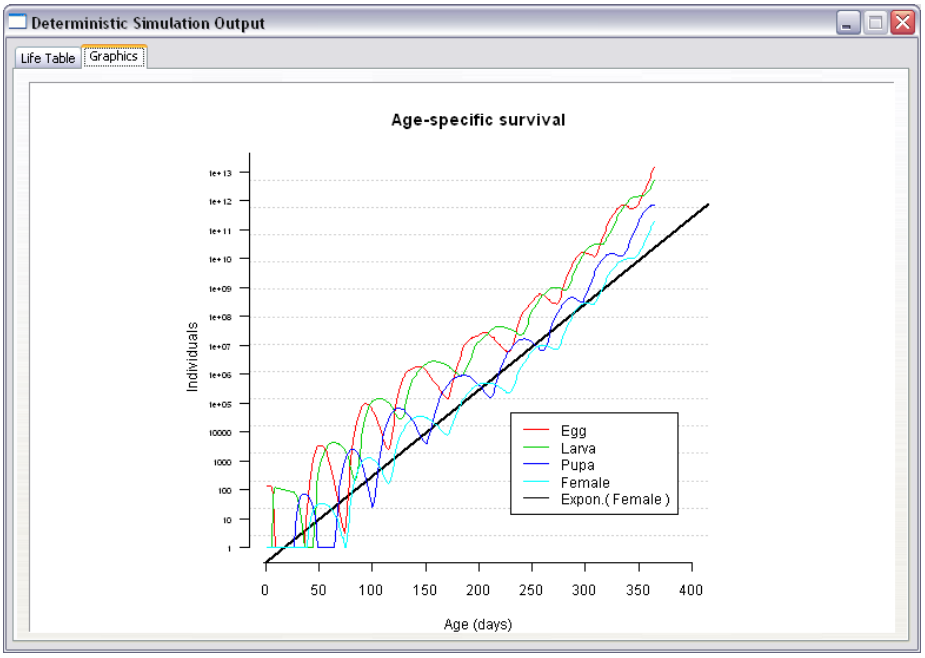
Click on the **"*Create Life-Table*"** button, the application will simulate a life-table with the loaded data and the following window will appear.



ii) Output graph

Click on ***view graphic button*** to plot the population development and growth curves. As a result of this operation, the figure below displays the evolution of number of individuals for each life stage over time. The simulation started with 100 eggs. Over time, these eggs passed through different life stages or dies. When the population contains adult female (in this example first females emerges after about 80 days) new eggs are added to the population through

oviposition (reproduction). First generations can be differentiated by the waves described by lines; however, with each new generation the overlap of generations increases. Once the population's structure stabilized, the figure would show straight lines for each life stages.

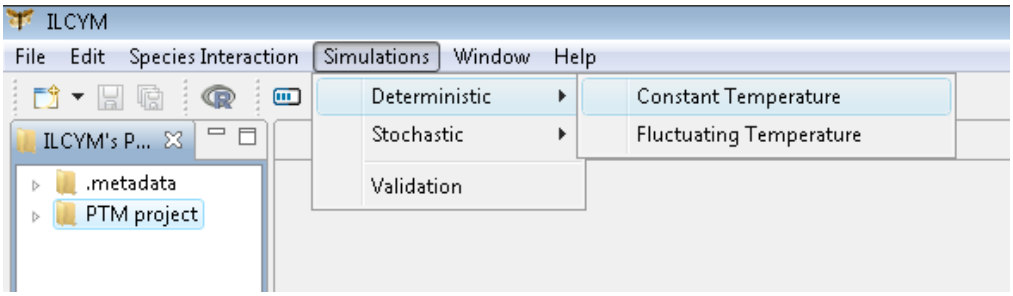


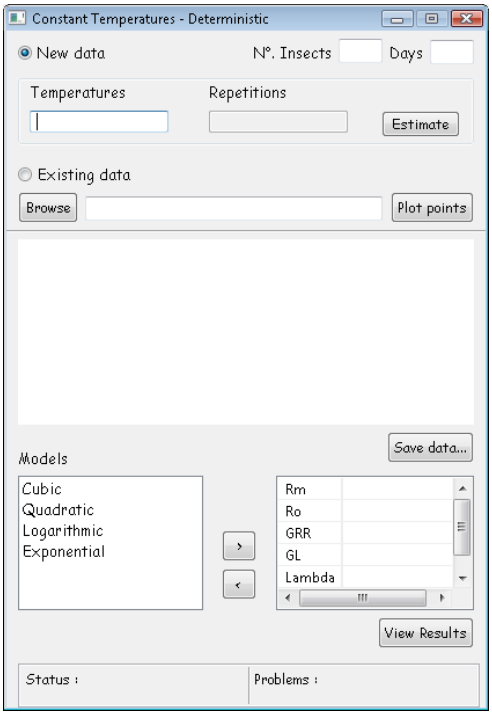
iv) Modifying the scale of the graphs

The user could right click on the image and the following window will appear

Here the user can modify the legend's coordinates, scales and the graph title.

As in stochastic simulation, this simulation can also be conducted at several constant temperatures at the difference that the user simply input the number of temperatures with no repetitions because the result will always be the same.





Note: In these simulations, always remember to input temperature values within the range that the insect under investigation can properly develop, if you input a temperature that is not suitable for development, ILCYM will output **NA** for life table parameter values

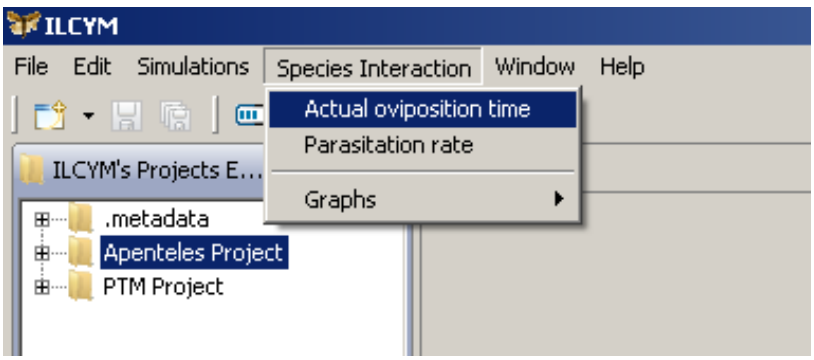
3.2.4 Species interactions

This section explains how two phenology models for distinct species (a host and a parasitoid) can simultaneously be simulated. The process here is deterministic and the algorithm used is the same as in single species simulation explain earlier. For demonstration of the simulation steps and outputs, the phenology models of the potato tuber moth *Phthorimaea operculella* (Zeller) (Lepidoptera: Gelechiidae) and its larva parasitoid *Apanteles subandinus* Blanchard (Hymenoptera: Braconidae) were chosen.

i) ***Actual oviposition time***

In ILCYM, the first step in conducting simulation of interacting species is to evaluate the actual oviposition time of the female parasitoid which, is defined as the exact length of the oviposition period. This quantity is different to the time span between first oviposition and oviposition of the last egg.

To estimate this parameter, go to window, then open perspective, select validation and simulation. Under species interaction, select actual oviposition time as shown below.

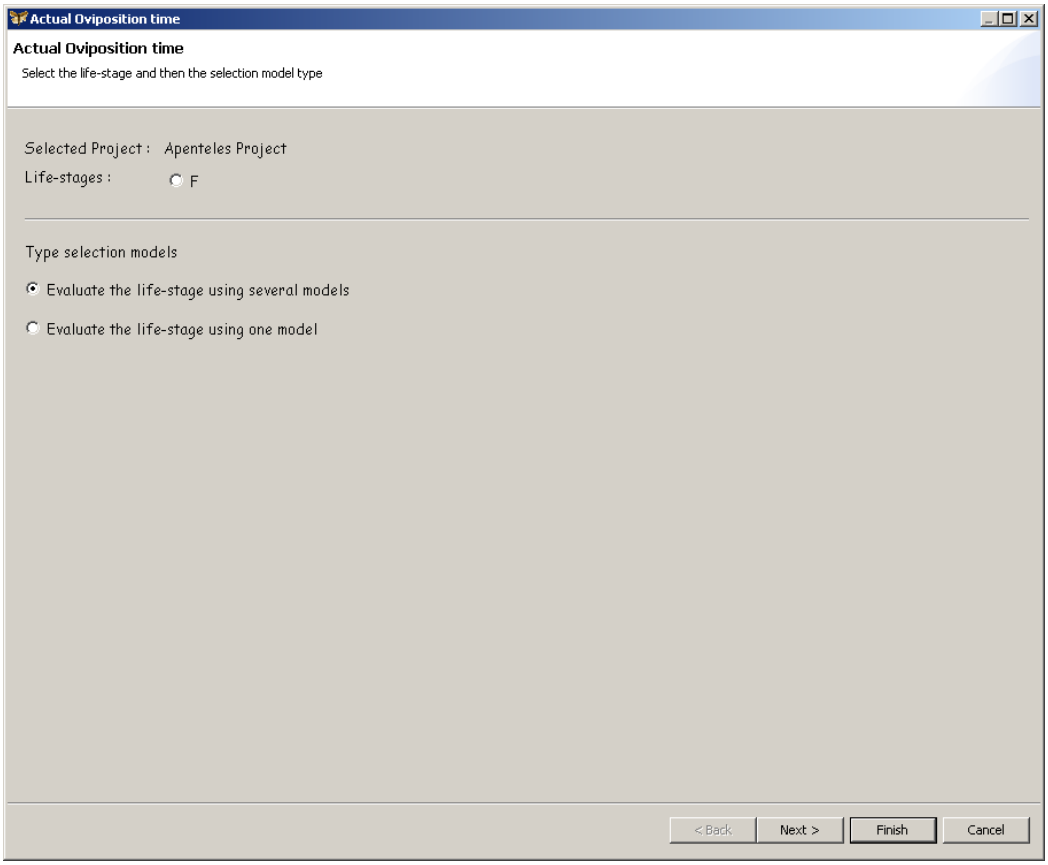


In this example, ILCYM's projects window contains two projects:

PTM project: standing for *Phthorimaea operculella*

Apanteles project: *designating Apanteles subandinus project.*

After clicking on actual oviposition time, the window below will appear, select female represented by ***F*** and proceed with the analysis by clicking the ***next bottom***


Actual Oviposition time
Actual Oviposition time
Select the life-stage and then the selection model type
Selected Project : Apenteles Project
Life-stages : F
Type selection models
Evaluate the life-stage using several models
Evaluate the life-stage using one model
< Back
Next >
Finish
Cancel

Selected project: Apanteles project

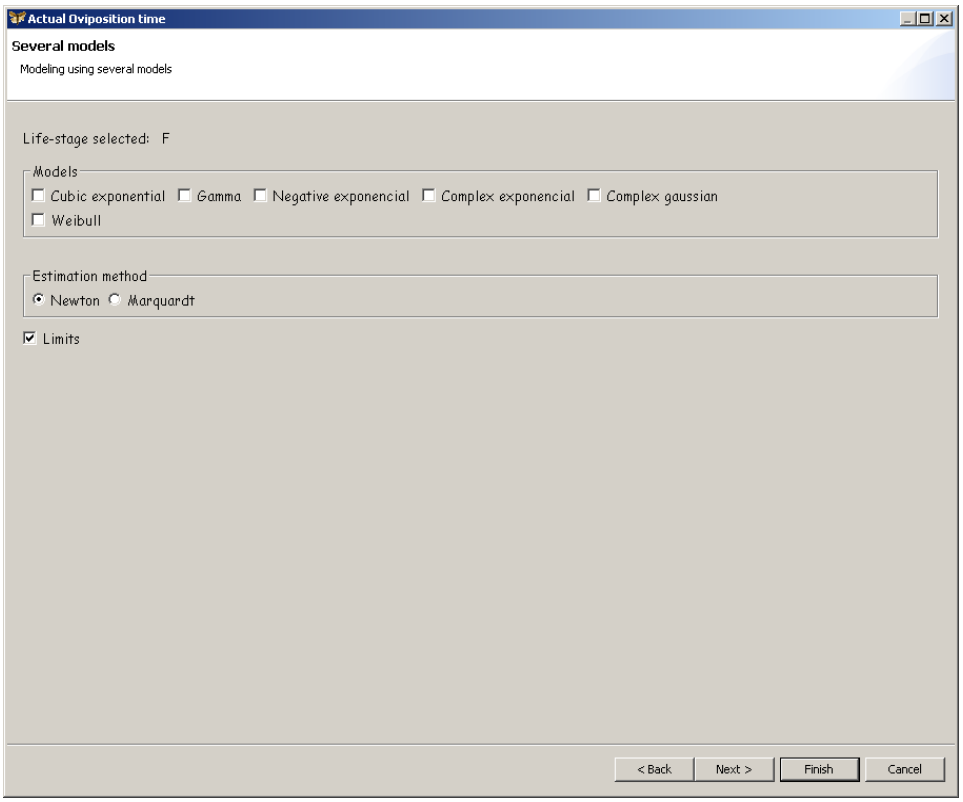
Life stages: select the life stage, ***F*** means female

Type selection models: You should select one of the options

Evaluate the life-stage using several models

Evaluate the life-stage using one model

For example, if the option ***evaluate the life-stage using several models*** is choose, the window below shows different functions that can be fitted for estimating actual oviposition time. The process of selecting the best fitted model is identical as in the previous section of this manual.

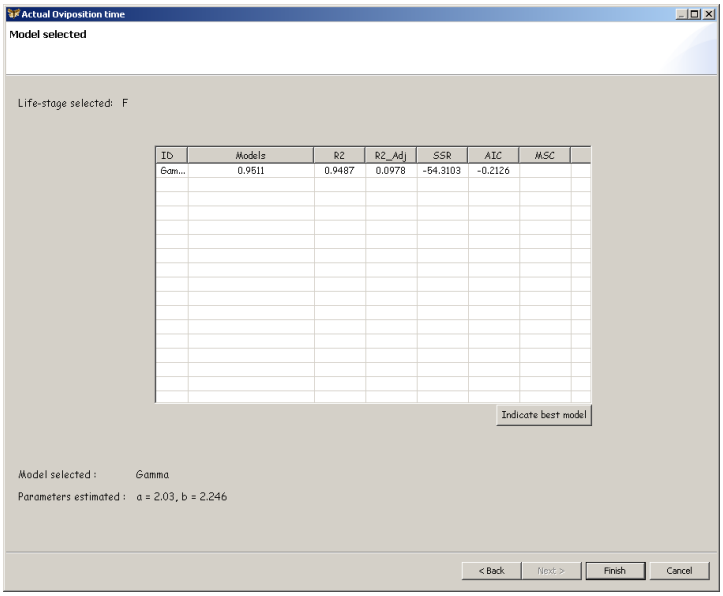


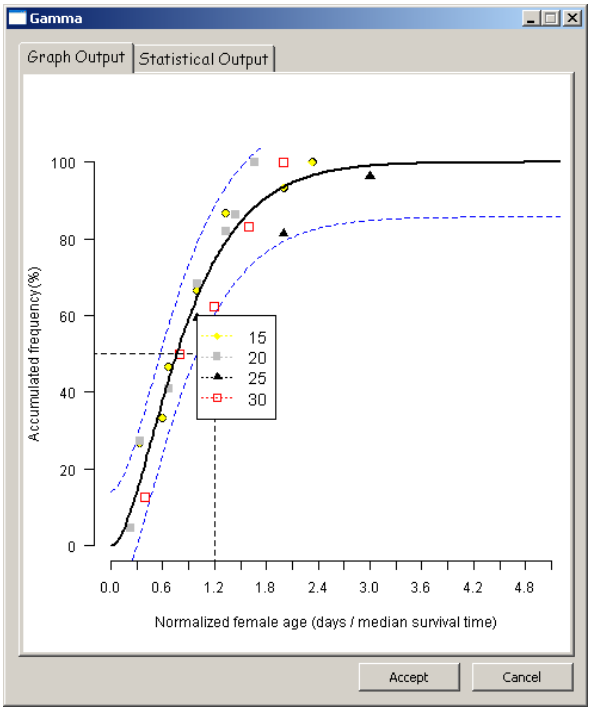
Life stage selected: F stands for female

Models: display name of the mathematical expressions available

Estimation method: stand for minimization algorithm.

The windows below display the statistical values and the graph of the selected model representing ***actual oviposition time***

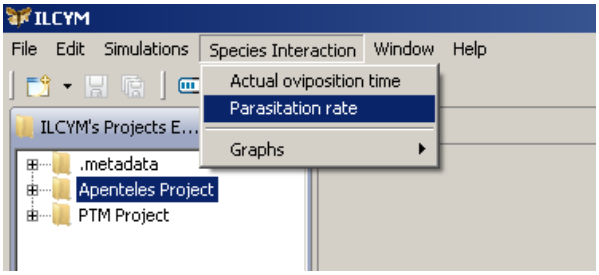




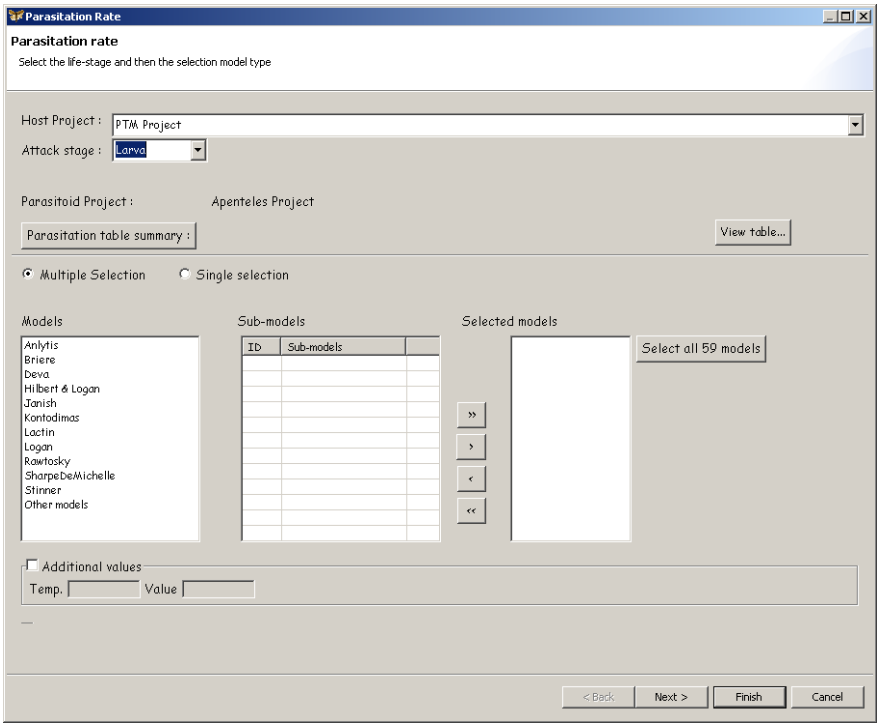
ii) ***Parasitation rate***

Parasitation rate is used in ILCYM to designate parasitism rate, this quantity maybe constant or temperature dependent. In case you choose to consider it as a factor of temperature, you will need to fit a nonlinear function to represent its variation with temperature.

Under species interaction ***click*** on ***parasitation rate*** as shown below



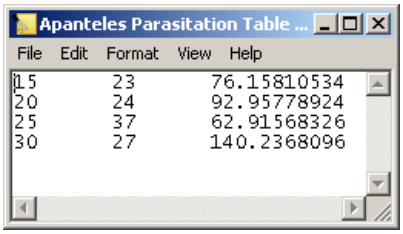
The window below will appear, go to the right of the host project ***combo*** and select the ***host project***, then select the ***attack stage*** and input the parasitation table



Host project: PTM project for this example

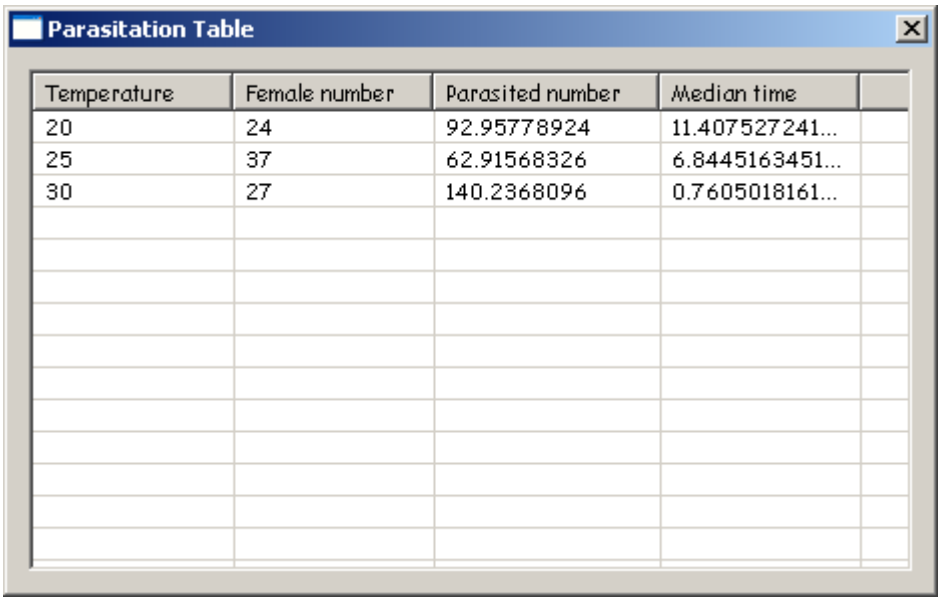
Attack stage: Larva (*Apanteles subandinus is a larva parasitoid for Phthorimaea operculella)*

Parasitation table summary: Click on this bottom to select the location on your computer where the table summary of parasitation is store. A sample table format is display below

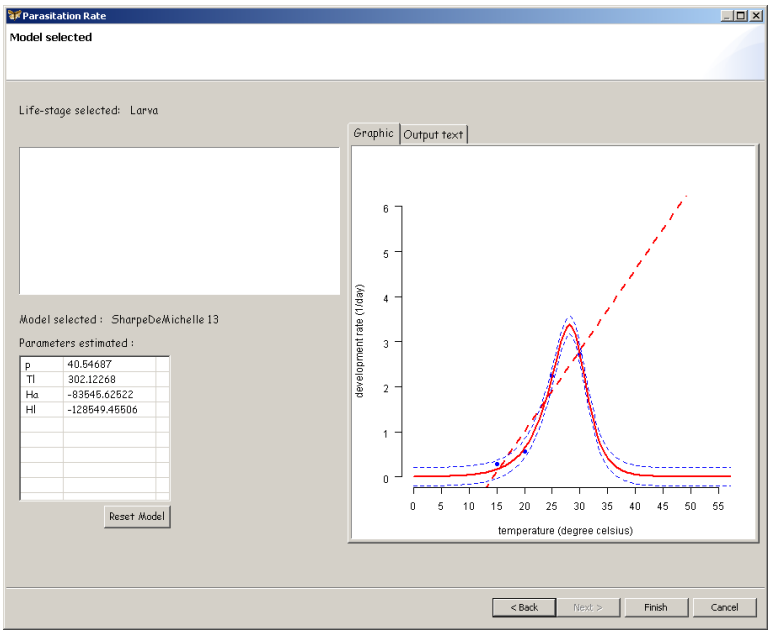


In this table the first column designate the temperature, the second column is the number of female parasitoid and the third column is the number of host parasitized.

View table: Once the table is loaded, you can view the table by clicking on ***view table bottom***, the table below will be display. This new table contains the same information as the input parasitation table however with an added column displaying ***median actual oviposition time***. The values of median development time were internally estimated.

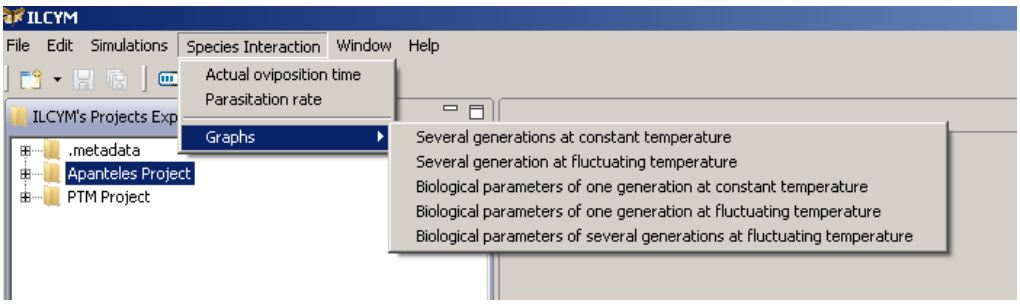


After inputting all information, you can click on multiple or single selection and then choose the best fitted model for parasitism following the same procedure as in previous sections (e.g developmental rate). The window also provides space for additional values. Once the fitting process completed, a window such as below will appear displaying the selected sub-models for parasitism.



Note: The steps described above are only necessary for variable parasitation rate

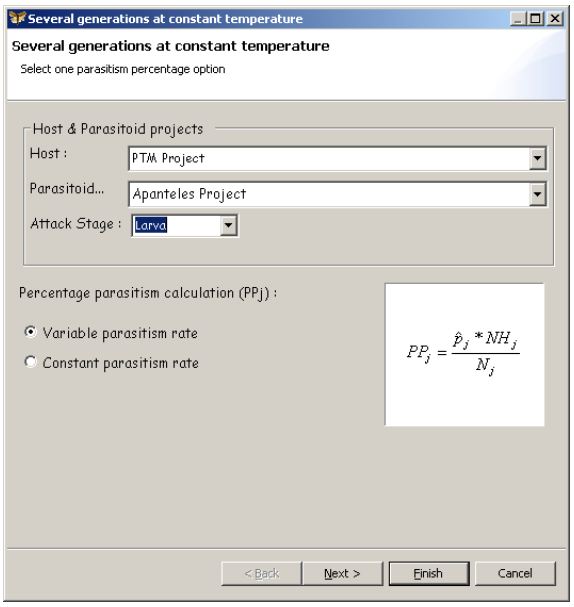
Under species interaction, go to graph, a menu will appear with distinct analysis:



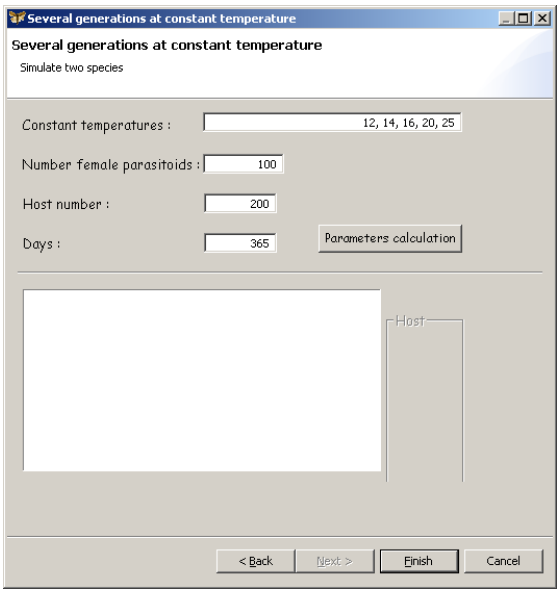
Note: For these simulations, users will be requested to input different number of hosts and parasitoids. As the numeral proportion of these species varies, you will study possible efficiency of a particular parasitoid in controlling a host pest.

Several generations at constant temperature

Choosing this option will allow you to simulate an insect host and its parasitoid within a designated time frame at constant temperature. By clicking on the extreme right of the ***combo box***, you can select your insect host and parasitoid projects, then specify the ***attack stage*** and ***click next***.



After clicking next, the following window will appear.



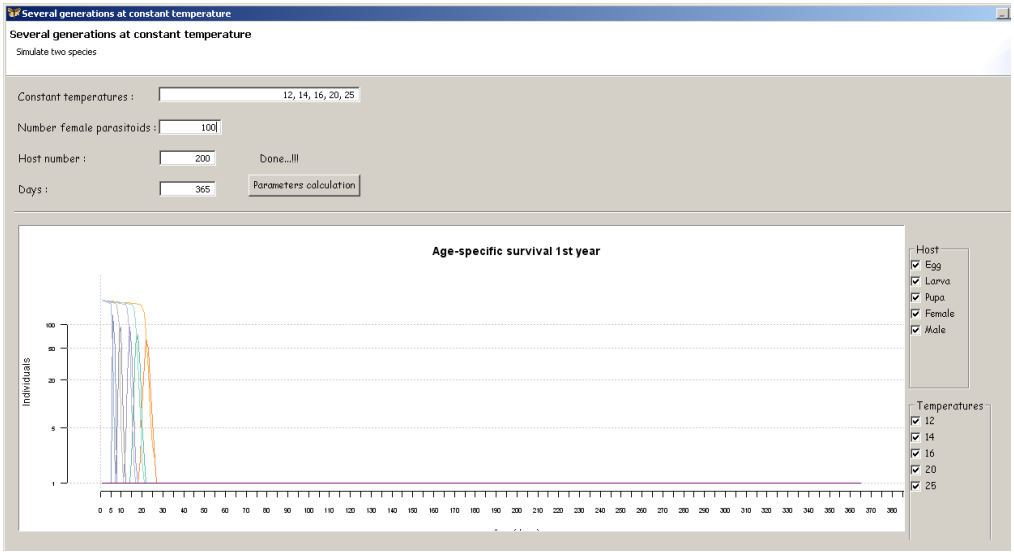
Constant temperature: input the temperatures for which you desire to simulate your species (make sure these temperature are within the developmental ranges for both the host and its parasitoid)

Number female parasitoids: input the number of female parasitoids for the simulate

Host number: input the number of host that for the simulate

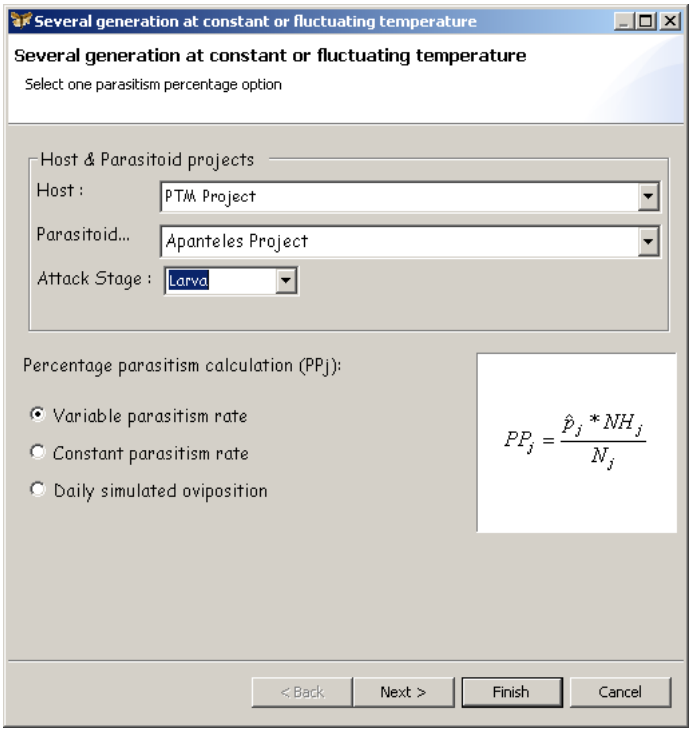
Days: number of day for the simulation, generally one year (365 days), you can also simulate just for the growing period of a particular plant.

Below is the sample output for the simulation results displaying the age specific survival for each stage of the insect host at each inputted temperature.



Several generations at fluctuating temperature

Once this option is selected, the window below will appear titled several generations at constant or fluctuating temperature meaning the analysis is conducted both under constant and fluctuating temperature.



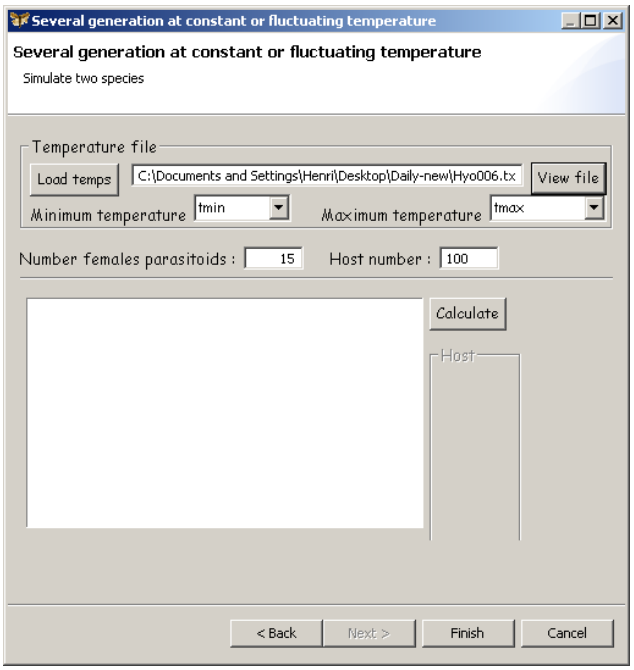
Three options are display under percentage parasitism calculation

Variable parasitism rate: refer to the variable parasitation rate; this option will be selected if you wish to consider that the parasitation rate is a function of temperature. Prior to its selection, you must make sure that a function representing parasitation rate has already been fitted and save.

Constant parasitism rate: refer to parasitation rate which is constant in value that does not depend to any variable.

Daily simulated oviposition: this option allows of linking both phenology model through the number of female parasitoid oviposited egg.

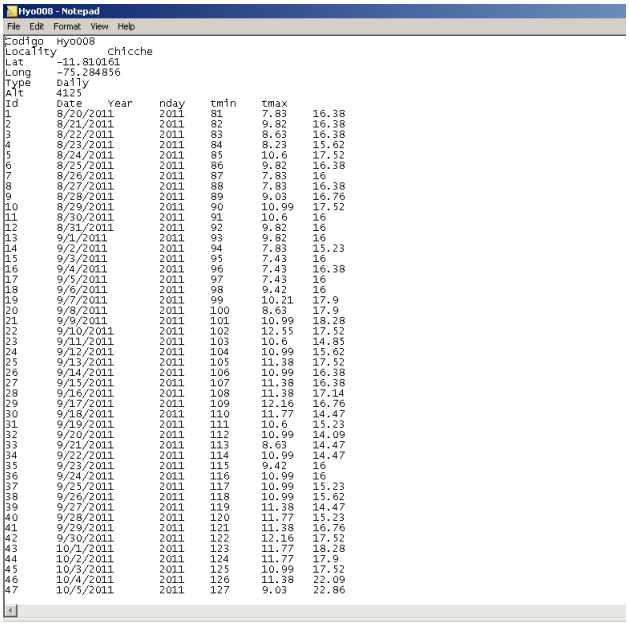
Click next and the window below will appear



Load temps: Allow you t load the temperature file

View file: for viewing the load temperature file

ILCYM'S input standard climate station file as shown below



Hyo008 - Notepad

File Edit Format View Help

```
Codigo  Hyo008
Locality        Chicche
Lat     -11.810161
Long    -75.284856
Type    Daily
Alt     4125
Id      Date    Year    nday    tmin    tmax
1       8/20/2011       2011    81      7.83    16.38
2       8/21/2011       2011    82      9.82    16.38
3       8/22/2011       2011    83      8.63    16.38
4       8/23/2011       2011    84      8.23    15.62
5       8/24/2011       2011    85      10.6    17.52
6       8/25/2011       2011    86      9.82    16.38
7       8/26/2011       2011    87      7.83    16
8       8/27/2011       2011    88      7.83    16.38
9       8/28/2011       2011    89      9.03    16.76
10      8/29/2011       2011    90      10.99   17.52
11      8/30/2011       2011    91      10.6    16
12      8/31/2011       2011    92      9.82    16
13      9/1/2011        2011    93      9.82    16
14      9/2/2011        2011    94      7.83    15.23
15      9/3/2011        2011    95      7.43    16
16      9/4/2011        2011    96      7.43    16.38
17      9/5/2011        2011    97      7.43    16
18      9/6/2011        2011    98      9.42    16
19      9/7/2011        2011    99      10.21   17.9
20      9/8/2011        2011    100     8.63    17.9
21      9/9/2011        2011    101     10.99   18.28
22      9/10/2011       2011    102     12.55   17.52
23      9/11/2011       2011    103     10.6    14.85
24      9/12/2011       2011    104     10.99   15.62
25      9/13/2011       2011    105     11.38   17.52
26      9/14/2011       2011    106     10.99   16.38
27      9/15/2011       2011    107     11.38   16.38
28      9/16/2011       2011    108     11.38   17.14
29      9/17/2011       2011    109     12.16   16.76
30      9/18/2011       2011    110     11.77   14.47
31      9/19/2011       2011    111     10.6    15.23
32      9/20/2011       2011    112     10.99   14.09
33      9/21/2011       2011    113     8.63    14.47
34      9/22/2011       2011    114     10.99   14.47
35      9/23/2011       2011    115     9.42    16
36      9/24/2011       2011    116     10.99   16
37      9/25/2011       2011    117     10.99   15.23
38      9/26/2011       2011    118     10.99   15.62
39      9/27/2011       2011    119     11.38   14.47
40      9/28/2011       2011    120     11.77   15.23
41      9/29/2011       2011    121     11.38   16.76
42      9/30/2011       2011    122     12.16   17.52
43      10/1/2011       2011    123     11.77   18.28
44      10/2/2011       2011    124     11.77   17.9
45      10/3/2011       2011    125     10.99   17.52
46      10/4/2011       2011    126     11.38   22.09
47      10/5/2011       2011    127     9.03    22.86
```

When your climate station is loaded, you need to go to minimum temperature and maximum temperature to select *tmin* and *tmax* for your analysis.

Minimum temperature: click on the combo box and select *tmin*

Maximum temperature: click on the combo box and select *tmax*

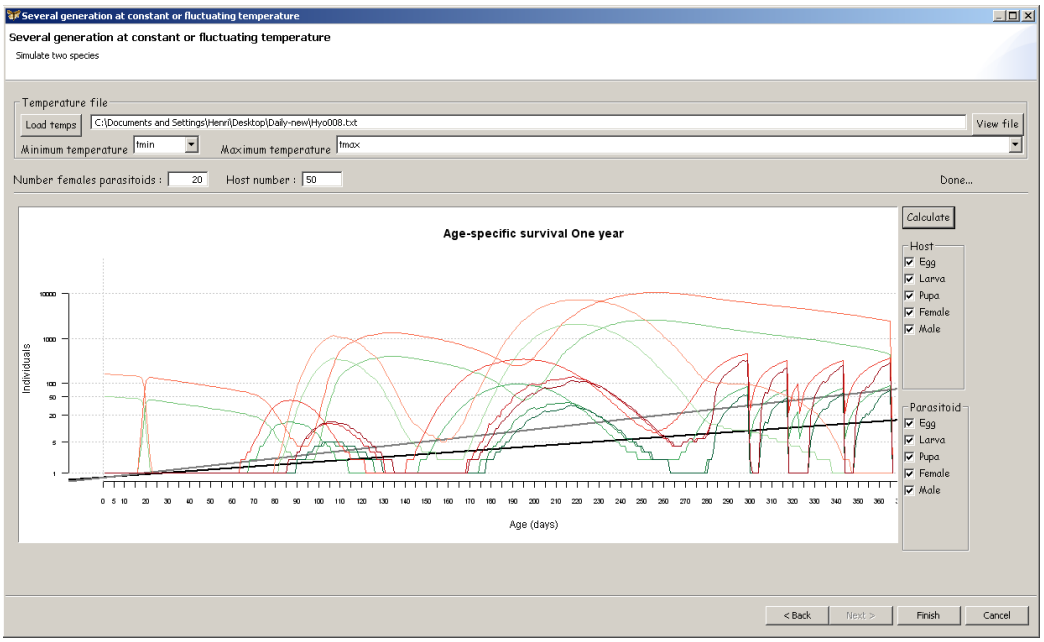
Number of female parasitods: input the number of female parasitoids

Host number: input the number of host

Calculate: for starting the simulation

The graph below is an example of a simulation of a PTM - *Apanteles* interacting system with a constant parasitation rate. The number of *Apanteles* is 20 with a fecundity of 8 for each individual; the total number of PTM is 50.

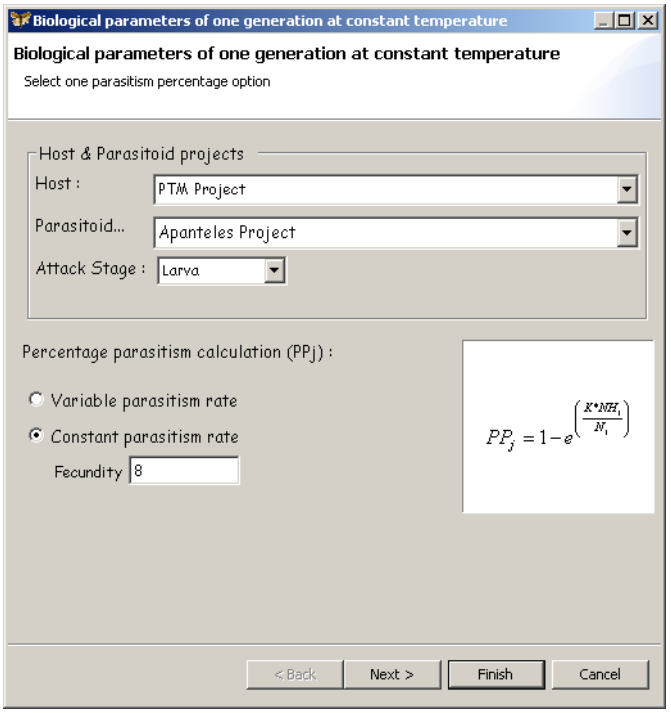
The release of natural enemies (parasitoids) against pests (hosts) is common in several integrated pest management systems and the basic precept of such practice is that parasitoid will contribute to reduce and stabilize the pest (host) population density. The proposed simulation can assist with the interpretation of the potential parasitoid efficiency in reducing and or stabilizing the host density for utilization in classical biological control. Such analysis can also assist in estimating the number of parasitoids that can be release for classical biological control purpose.

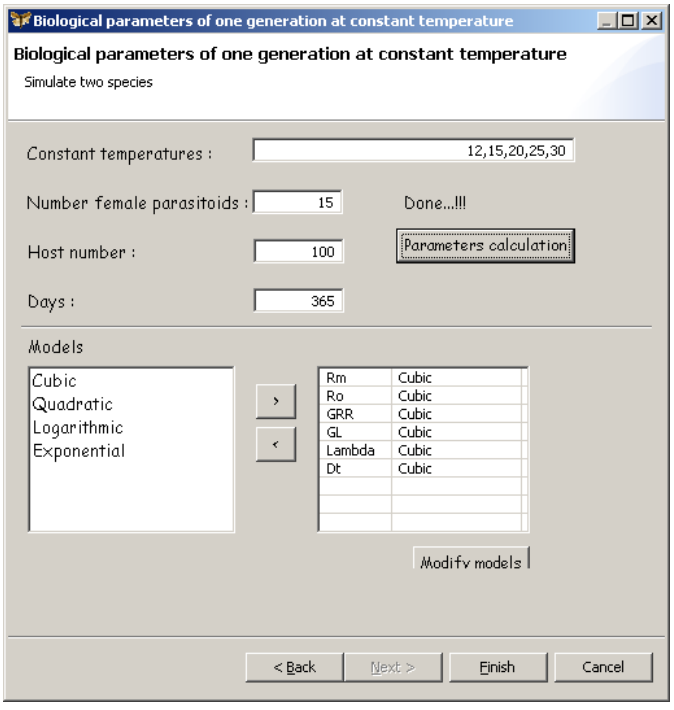


Biological parameters of one generation at constant temperature

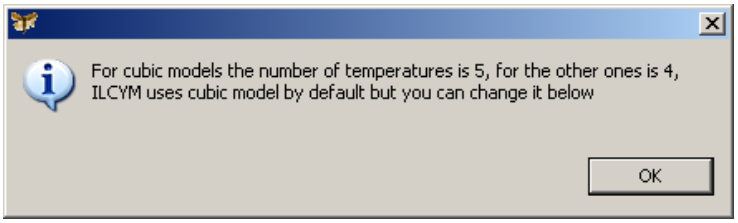
The biological parameters are referred to the life table parameters

Below is an example where a constant parasitism rate was selected with a fecundity of 8.

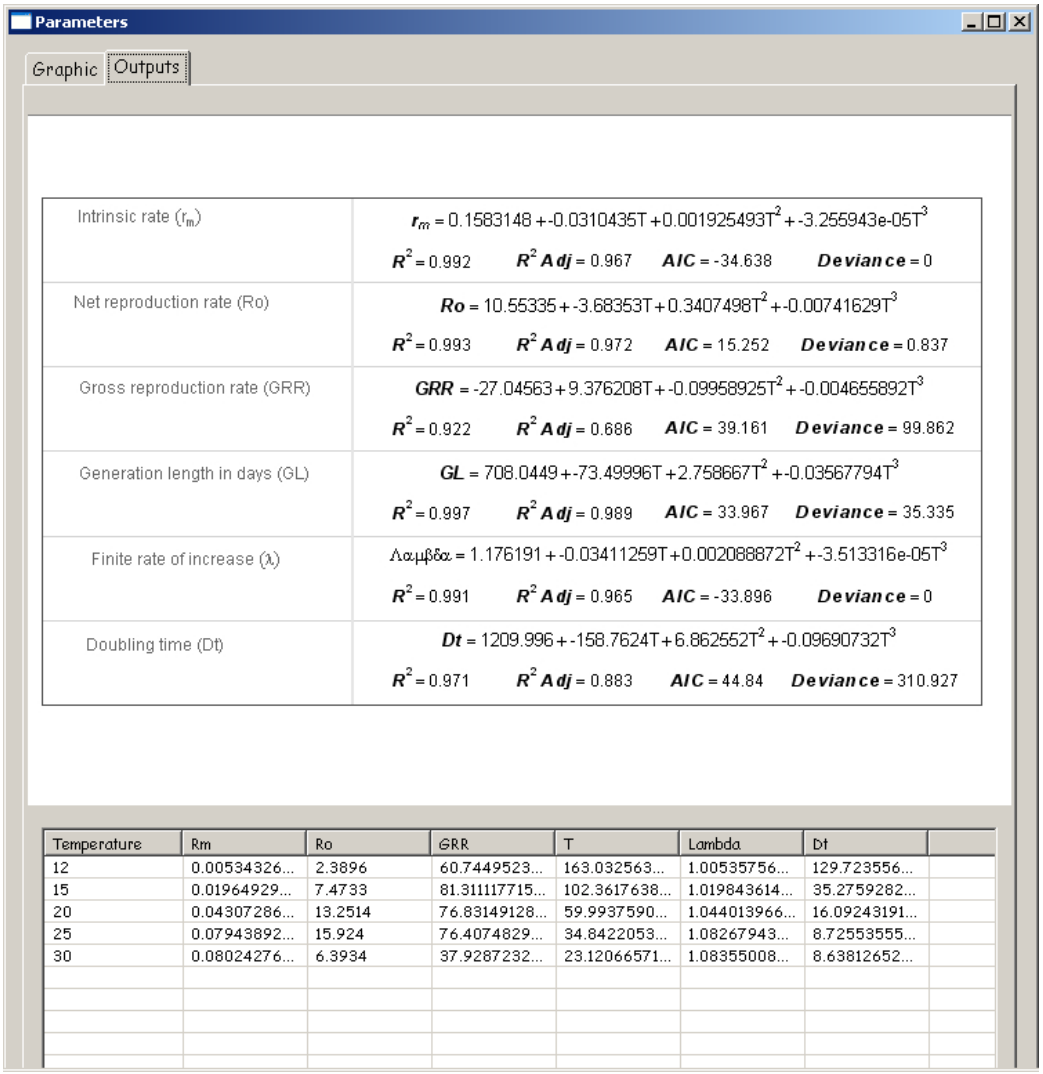


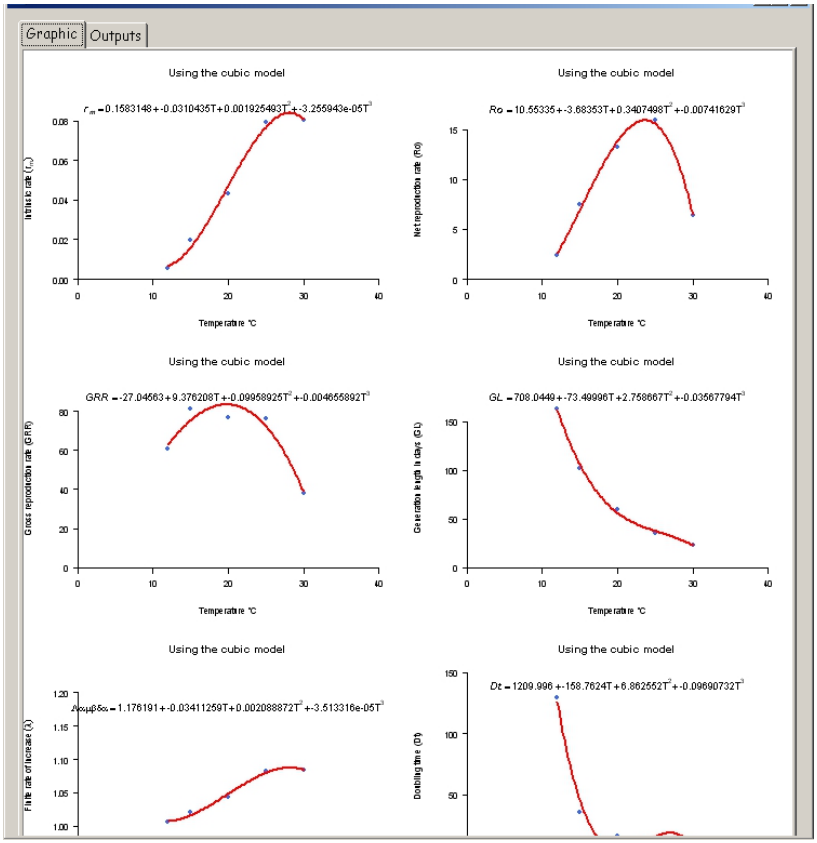


When the window below appear just click ok


For cubic models the number of temperatures is 5, for the other ones is 4,
ILCYM uses cubic model by default but you can change it below
OK

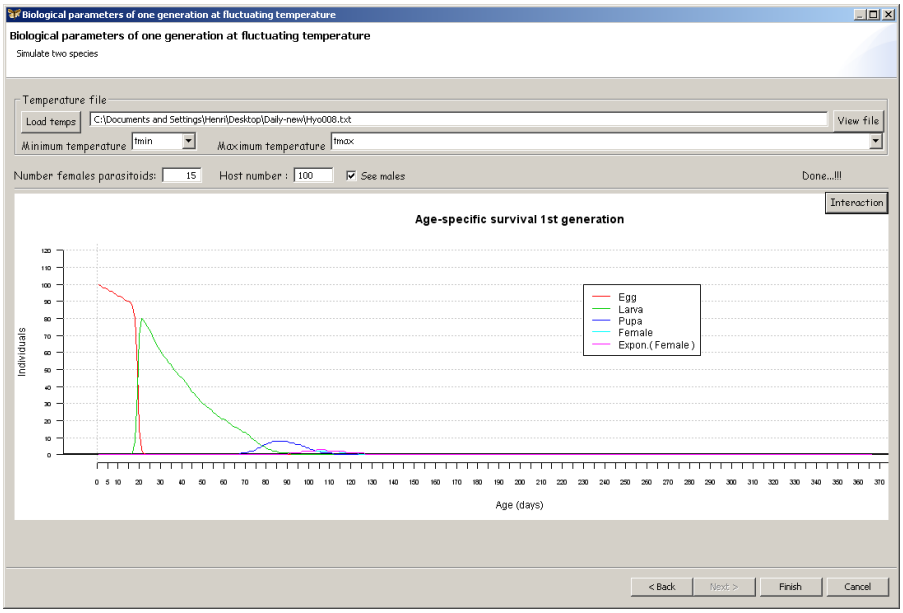
Below are ILCYM's outputs for different life table parameters of the insect host (PTM)





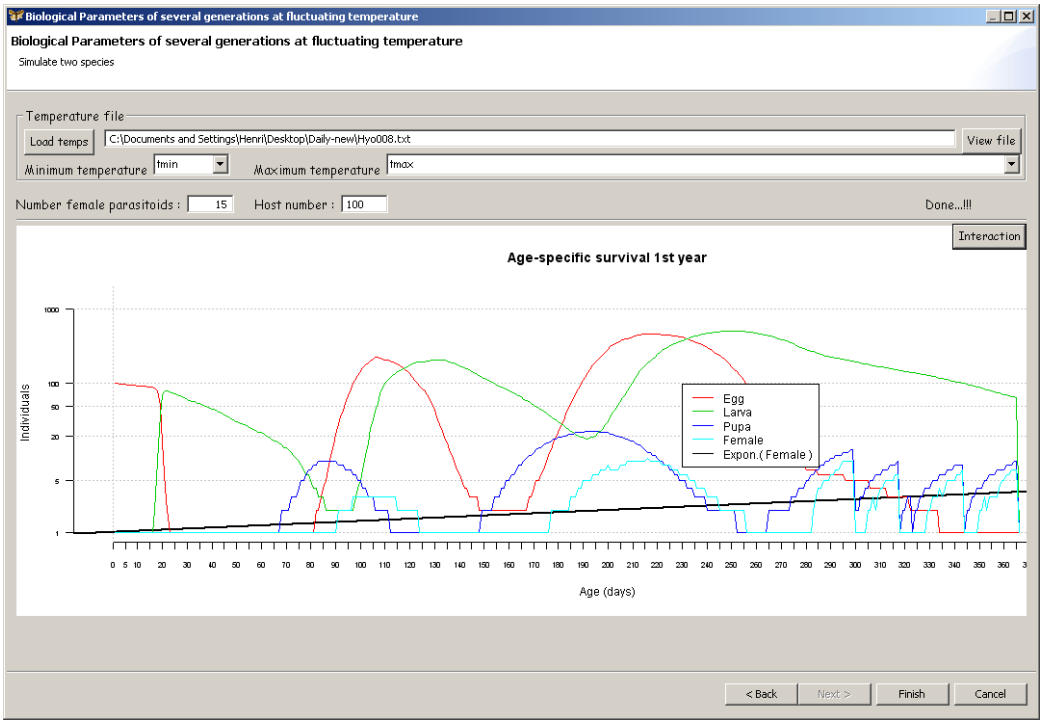
Biological parameters of one generation at fluctuating temperature

Just as for biological parameters of one generation at constant temperature, some analysis can be conducted under fluctuating temperature.



Biological parameters of several generations at fluctuating temperatures

This analysis allow you to visualize the host population after several generation within a time frame.



3.3 Potential Population Distribution and Mapping

Populations are spatially simulated through grid-based within a defined area according to grid-specific daily temperatures interpolated from available databases. If the study insect is a pest, the tool can plot indices based on simulation results for visualizing the establishment risk, the spread and damage potential of that pest species on a map.

3.3.1 Climate data

ILCYM can simulate maps at different resolution p.e. 10 minutes which is equivalent of 18 x 18 Km, 5 minutes equal to 9 x 9 km, 2.5 minutes equal to 4.5 x 4.5 Km and 30 seconds that is equal to 0.9 x 0.9km. The lower resolution, for example 10 minutes, are used to map larger areas such as the whole word, highest resolutions give detailed information in the map, ILCYM's climate input data are in ***.flt*** format.

a) Current temperature data

The temperature data used for spatial simulations (present scenario) were obtained from WorldClim available at http://www.worldclim.org/. The database is a set of global climate layers (grids) with different spatial resolutions that contains monthly average minimum, maximum and mean temperatures that were interpolated from historical temperature records worldwide (NOAA data) between 1950 and 2000. The data are well documented in Hijmans et al. (2005). For spatial population simulations and model output validations at different locations (point by point) temperature data directly obtained from local weather stations can be used.

b) Future temperature change data

For simulating population parameters for *P. operculella* for the year 2050 (climate change scenario) ILCYM's input downscaled data to project temperature changes. The predictions based on the WorldClim database are described by Govindasamy et al. (2003). The downscaling of data which was conducted by Ramirez and Jarvis (2010) is freely accessible at http://gisweb.ciat.cgiar.org/GCMPage. ILCYM's was also adapted to input

temperature datasets from other sources such as CliMond data base used in CLIMEX software.

c) Temperature data format

The data from WorldClim and majority of available data sources are in ***ascii***, **bil** or ***ArcGIS*** raster files. However ILCYM uses ***.flt*** data format (float type). When running the potential population mapping in ILCYM you need to convert your input data file in ***.flt*** using the following steps:

i) Converting ascii file in *.flt*:

- **Step 1:** Open ILCYM under Potential Population Distribution and Mapping perspective.
- **Step 2:** Click on import raster files
- **Step 3:** A window will appear, check ***ascii***.
- **Step 4:** Click on input button and you load your ***ascii*** file.
- **Step 5:** Click on output button and write were you want to save your ***.flt*** file.
- **Step 6:** Click import.

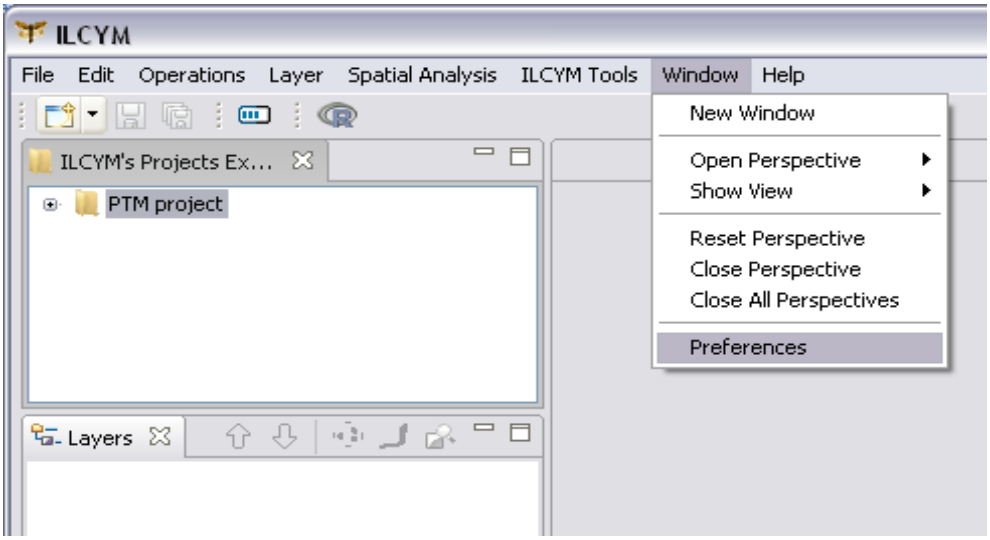
ii) Converting *bil* file in *.flt*:

- **Step 1:** Open ILCYM under Potential Population Distribution and Mapping perspective.
- **Step 2:** Click on import raster files
- **Step 3:** A window will appear, check ***bil***.
- **Step 4:** Click on input button and you load your ***bil*** file.
- **Step 5:** Click on output button and write were you want to save your ***bil*** file.
- **Step 6:** Click import.

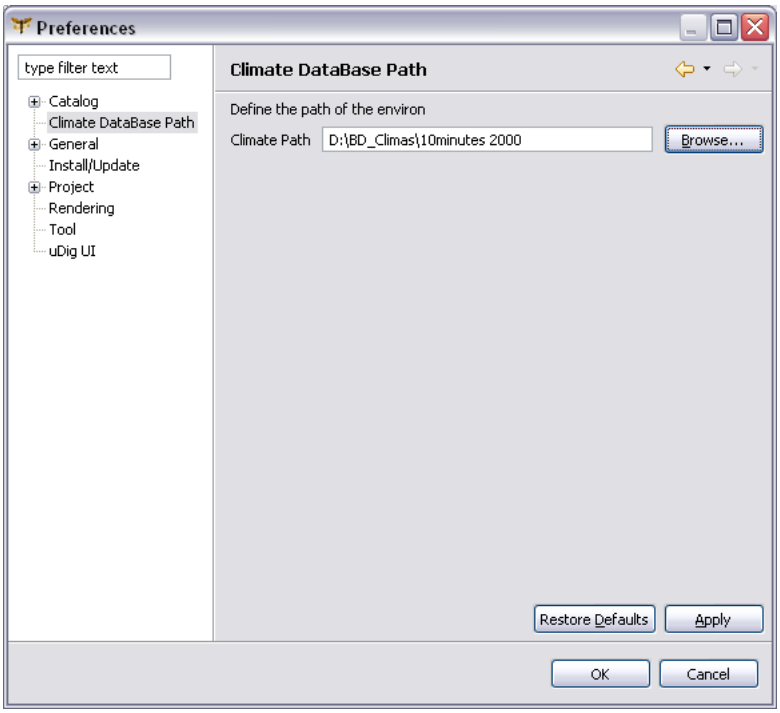
iii) **Converting *ArcGIS* raster files in *.flt*:** go to ArcGIS package and follow the instructions for converting ArcGIS Raster files to Float.

d) Setting the climate data base

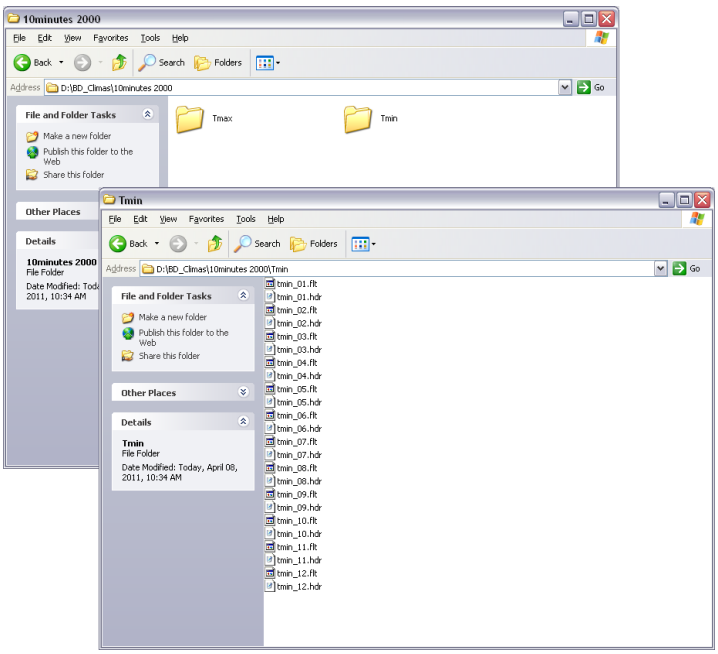
To set the climate data base in ILCYM, go to ***Window*** **menu**-> ***Preferences***-> ***Climate data base path*** **option**.



Select the path by clicking on ***Browse***, click on ***Apply*** **button** and the ***Ok*** **button**. Make sure you select the master folder that contains the ***Tmin*** and ***Tmax*** folders.

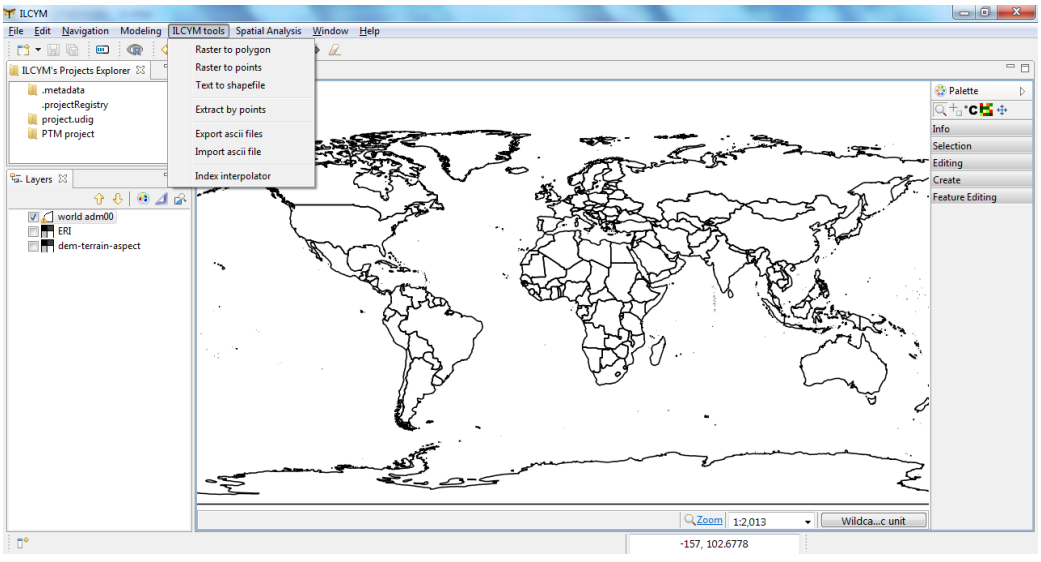


Below is the structure of the data, It has to be in two separate folders (one for ***Tmin*** and the other for ***Tmax***).



3.3.2 ILCYM Tools

A number of practical and analytical functions are available in ILCYM Tools menu. These functions allow you to create a shape file of points from a text file, extract data from climate database and convert grid from and to different GIS formats.



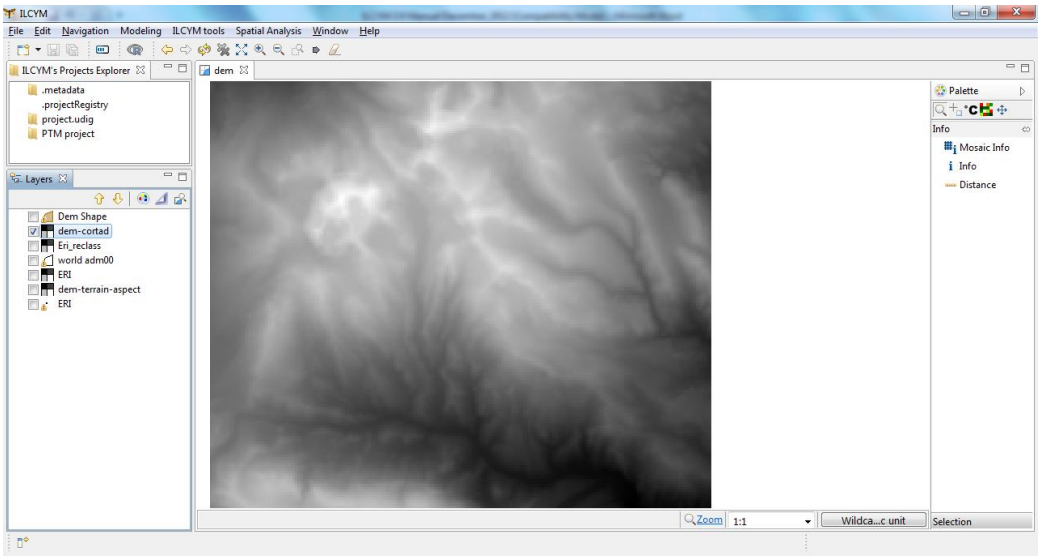
a) Raster to polygons

Convert a raster dataset to polygon

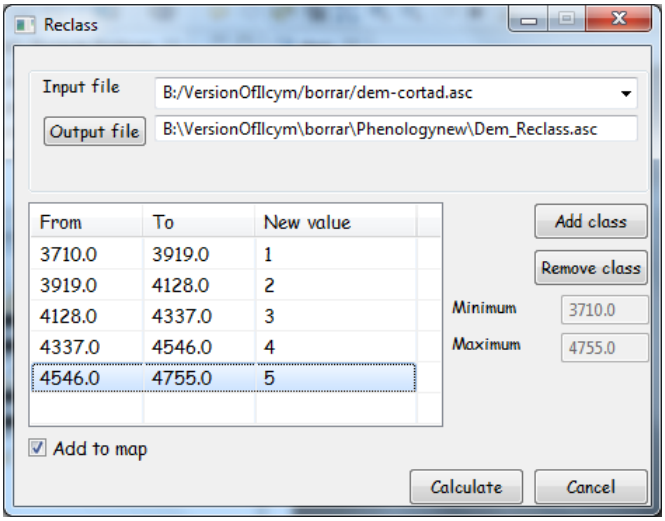
The input raster can have any cell size and must be a valid integer dataset. The cell values of the input raster (the VALUE field) will become a column with the heading “name of the raster” in the attribute table of the output feature class.

To better use this function, at first reclassify your raster (see Reclass function). This will allow you to change and classify the values in the raster. The final output may be useful for estimating areas of changes.

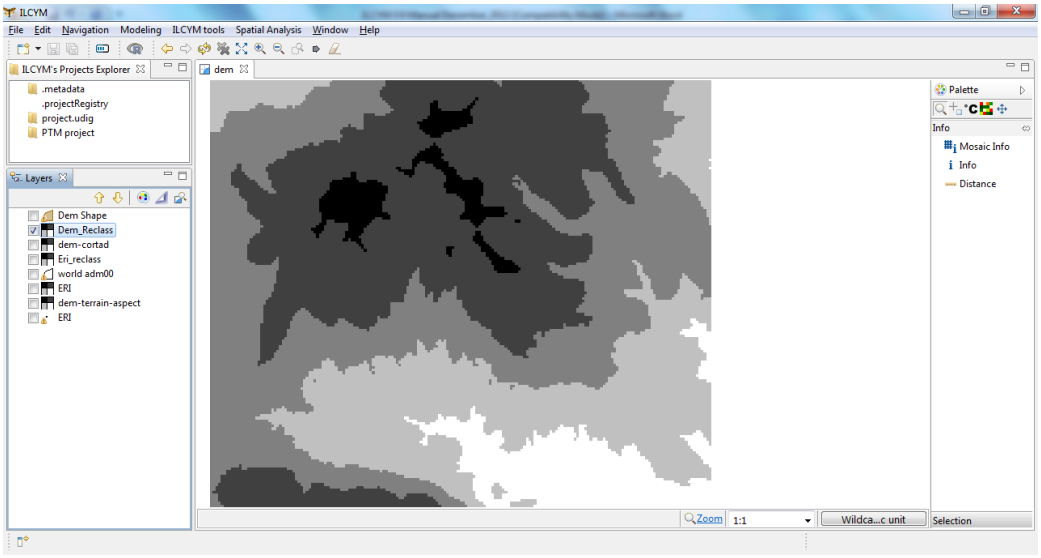
i) Load the raster file

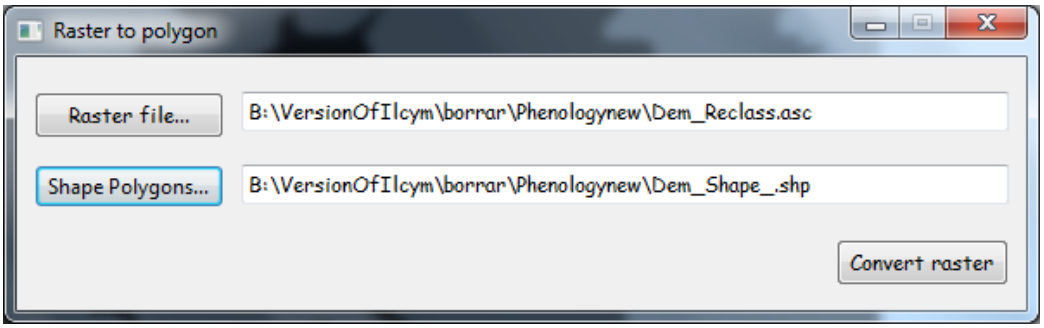


ii) Reclassify the raster file

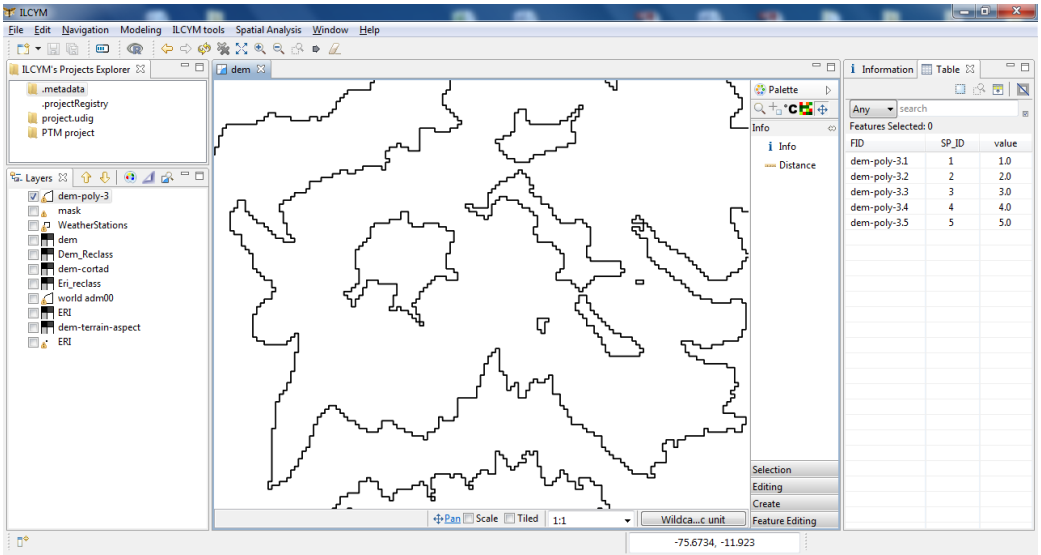


iii) Use the reclassify raster to convert to polygon





iv) Final result – Polygons and its attributes

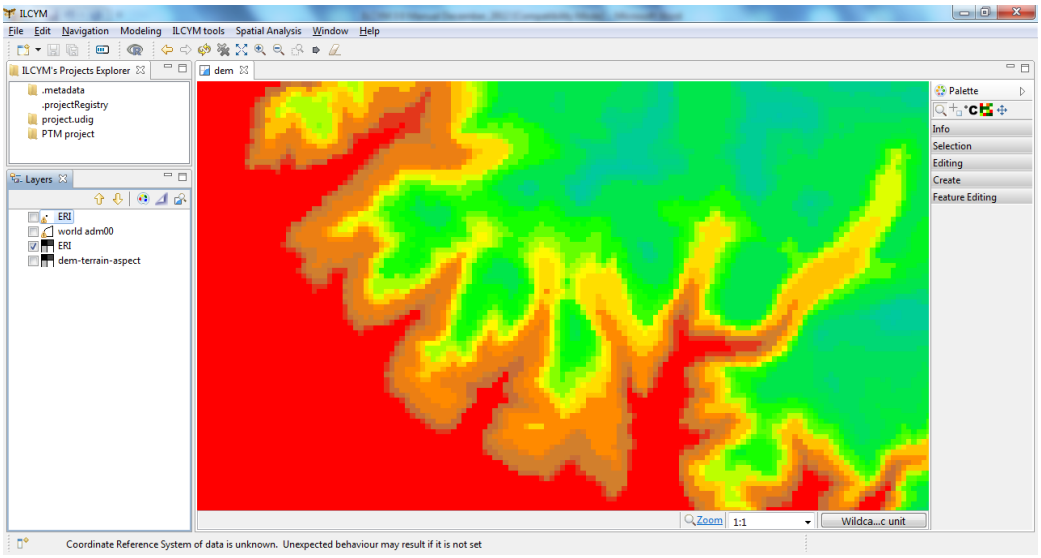


b) Raster to points

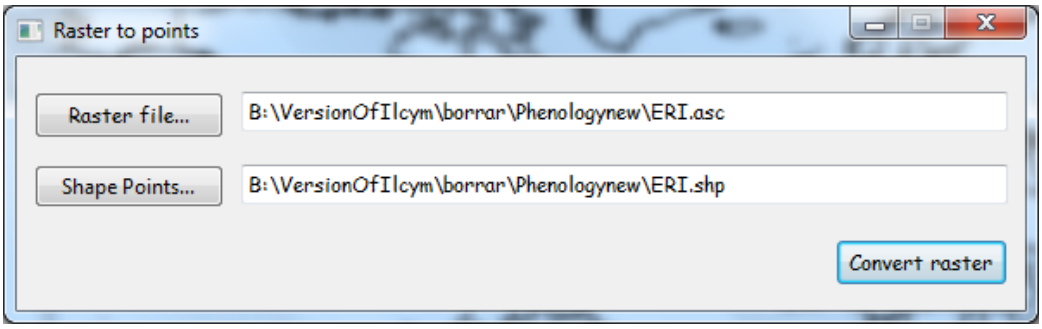
Converts a raster dataset to points

For each cell of the input raster dataset, a point will be created in the output feature class. The points will be positioned at the center of cells that they represent. The NoData cells will not be transformed into points. The input raster can have any cell size and may be any valid raster dataset.

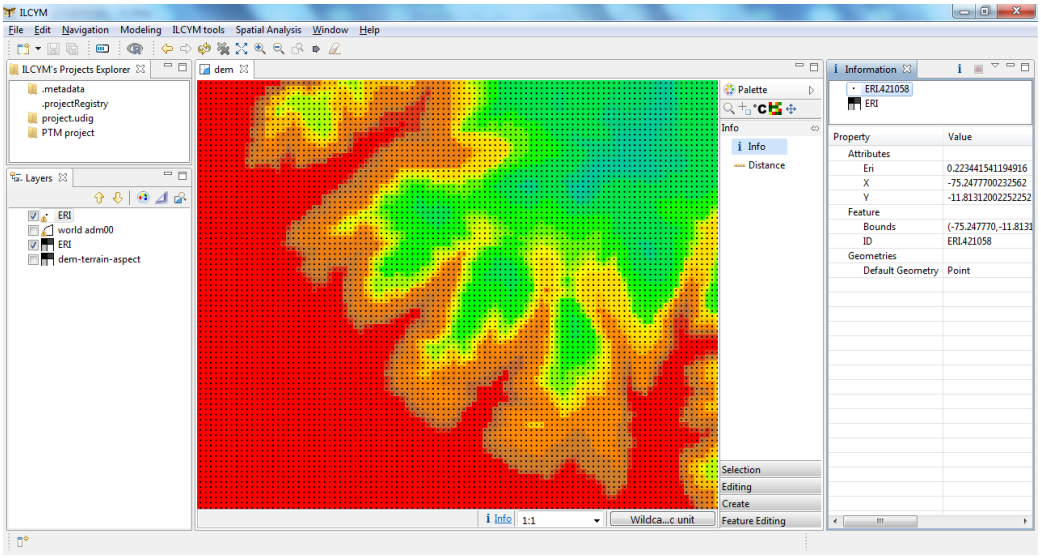
i) Load the raster that you wish to convert to points



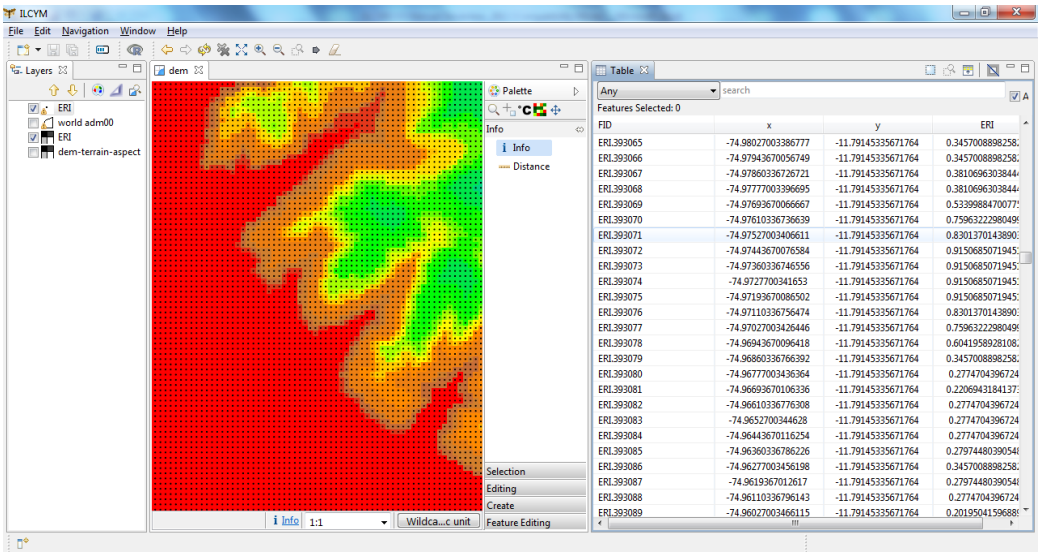
ii) Use the function raster to points



iii) Output points



iv) Output tables



c) Text file to shape file.

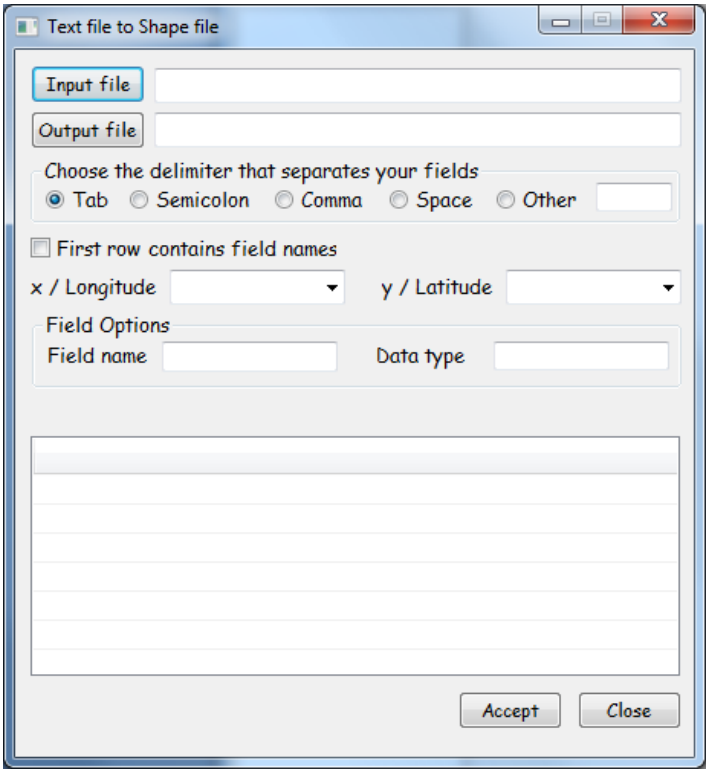
With this menu you can create a shape file of points from a text file that contains fields with latitude and longitude (both in decimal degrees). First, you must indicate the filename of your .***txt*** file and you have to provide the output filename of the new shape file.

The .***txt*** file must have a header row containing the variable names. It is preferable if the columns are separated by commas or tabs. The importation

wizard will read your data when you ***tick the box*** which specifies the separator you are using.

ILCYM will figure out what type of data is present in each column of the database: text, integer (whole) or real (decimal) numbers. But if you wish, you can change this automatically generated setting. The same goes for the maximum number of spaces that a value of the variable will need. If you indicate fewer spaces than they are actually used, the data will be truncated (cut off at the position that you indicated), not rounded.

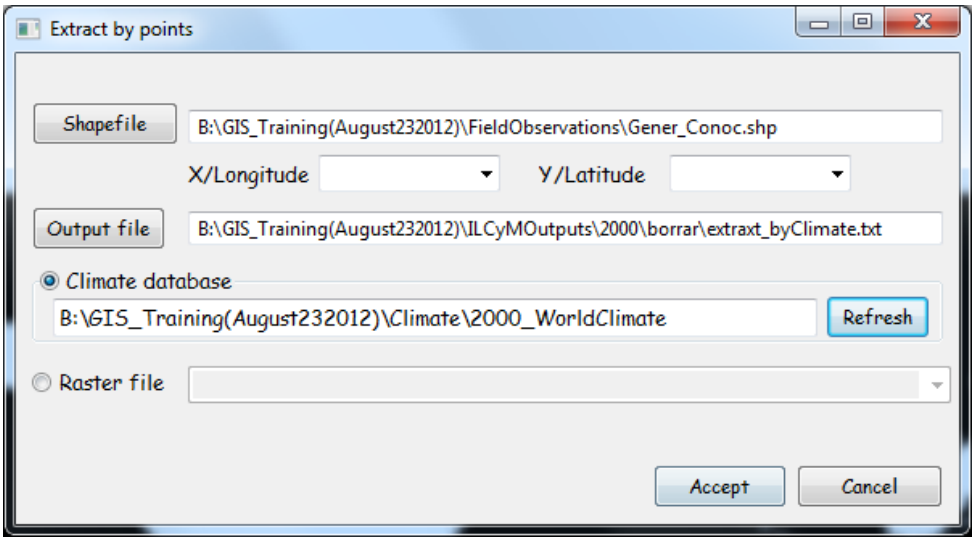
The program then reads the input file and allows you to select the fields that have the X (longitude) and Y (latitude) coordinate data. By default, only numerical fields are listed for you to choose from. When you do ***click on accept***, a new shape file of points is created.

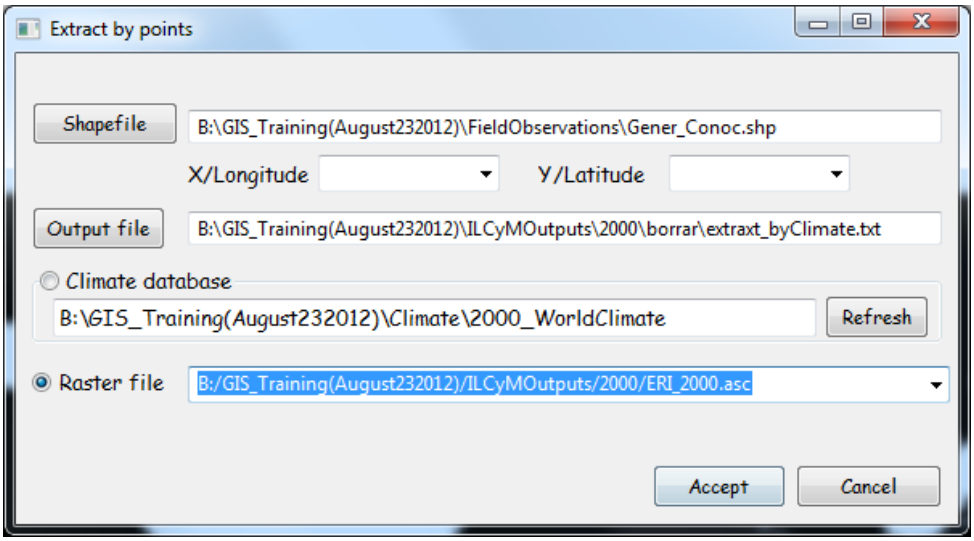


d) Extract by points

The Extract tool assigns values to the locations specified in the active point's shape file. You can extract values from a grid file or climate data. In all cases, the result is a text (***.txt***) file containing the fields of the original shape file plus de value of the grid where each dot is located.

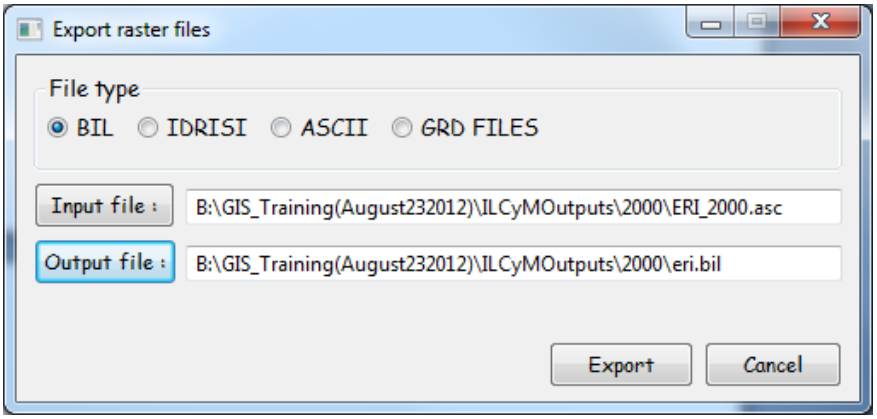
For example, if you have a shape file for a particular location, and you want to extract the values of the data points contained in your shape file, ***you click on shape file button*** and load the file, specify on ***output bottom*** where you want to save the new file. In doing this make sure the climate data base is uploaded.





e) Export Raster files

With the Export Raster files function you can export ILCYM ***ascii*** files to a number of different formats (.***bil***, ***Idrisi***, ***GRD Files***).

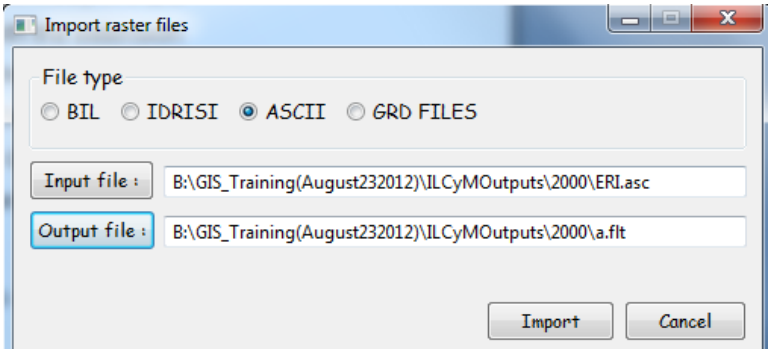


When exporting ***ascii*** files to the generic binary format .***bil*** ("band interleaved by line"), a data file with the extension .***bil*** is produced, as well as a header file with the extension **HDR**. These files can be imported into a number of GIS programs, including ***IDRISI, Arc/Info*** (with the "imagegrid" command) and ***ArcView*** (where they can be opened as an "image"). If you need a file in the similar formats **BIP** or **BSQ**, you can rename the extension of the output file, because these are the same when only one grid (or "band") is stored in a file.

When exporting grids to ***IDRISI*** (version 2 and earlier), the result is a data file with extension **IMG** and documentation file with extension **DOC**.

f) Import Raster files

With the Import Raster feature, you can import one raster into ILCYM from the IDRISI (**IMG** or **RST**), generic binary (**BIL**/**BIP**/**BSQ**), and **ESRI** binary export formats.



g) Index Interpolator

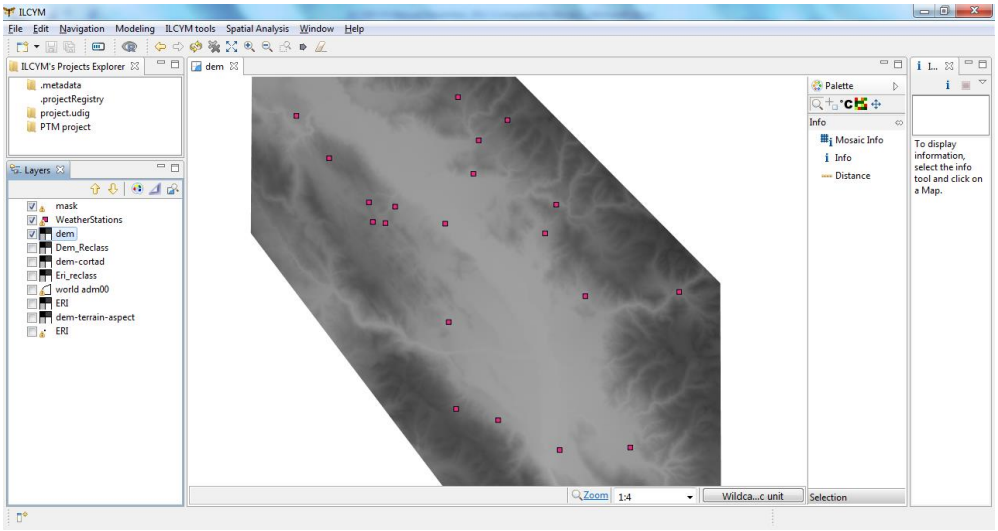
The assumption that makes interpolation a viable option is that spatially distributed objects are spatially correlated; in other words, things that are close together tend to have similar characteristics. The Index Interpolator tools create a continuous (or prediction) surface from sampled point values. You can measure hourly temperature at strategically dispersed sample locations, and predicted values can be assigned to all other locations. Input points can be either randomly or regularly spaced or based on a sampling scheme.

The interpolation tool makes predictions from sample measurements for all locations in an output raster dataset, whether or not a measurement has been taken at the location. There are a variety of ways to derive a prediction for each location; each method is referred to as a model. With each model, there are different assumptions made of the data, and certain models are more applicable for specific data. In the ***Index Interpolation***, we have implemented the “Thin plate algorithm” for interpolation.

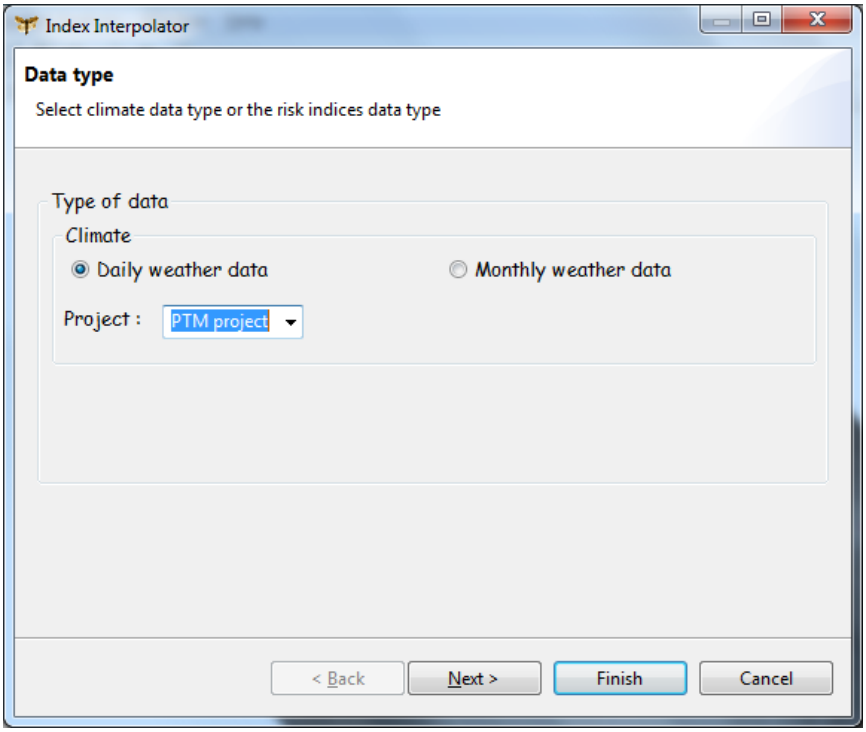
This sub-module module allows for the analysis of regional to local climate change patterns on pest establishment and abundance. This module inputs daily/montly minimum and maximum temperatures data, it calculate some index (see page 141) location by location and then applies the “Thin plate algorithm” for interpolation and output regional assessment.

When using the index interpolator, some important steps are required: geo-referencing the input data and then use digital elevation model for fitting your selected region, selection of your phenology model and the input data type, selection of the data of the weather stations, defining co-variables for the calculation and choice of the function used by thin plate algorithm.

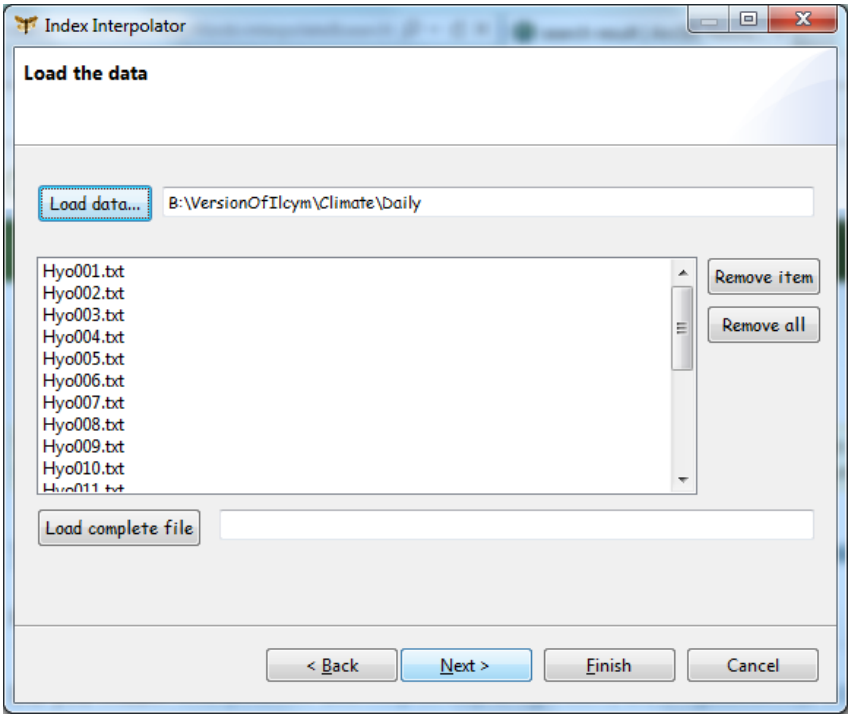
i) Geo-reference your inputs data and use a digital elevation model that fit in your region as shown below



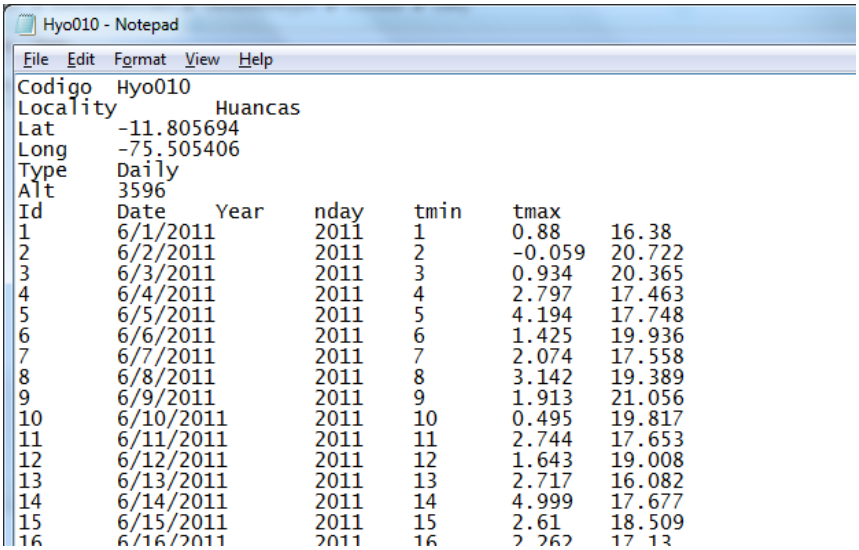
ii) Select your phenology model and your input data type



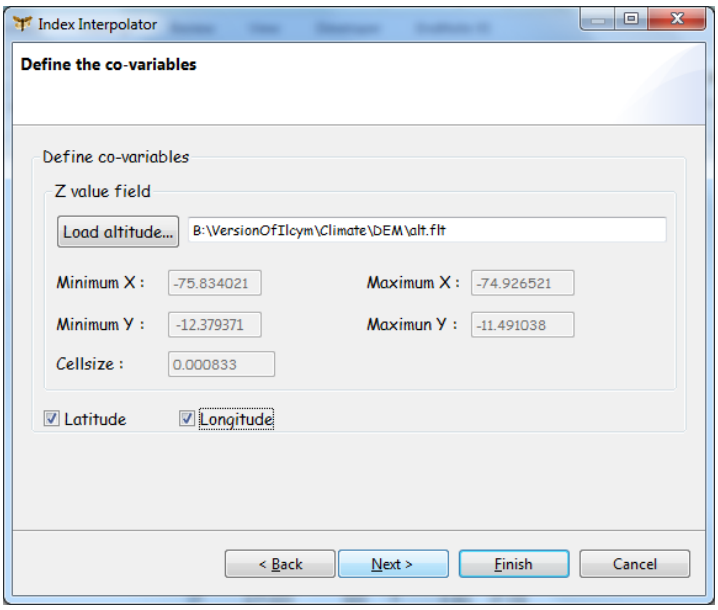
iii) Select the data for each weather station.



Note: Make sure each of your data file has the following structure

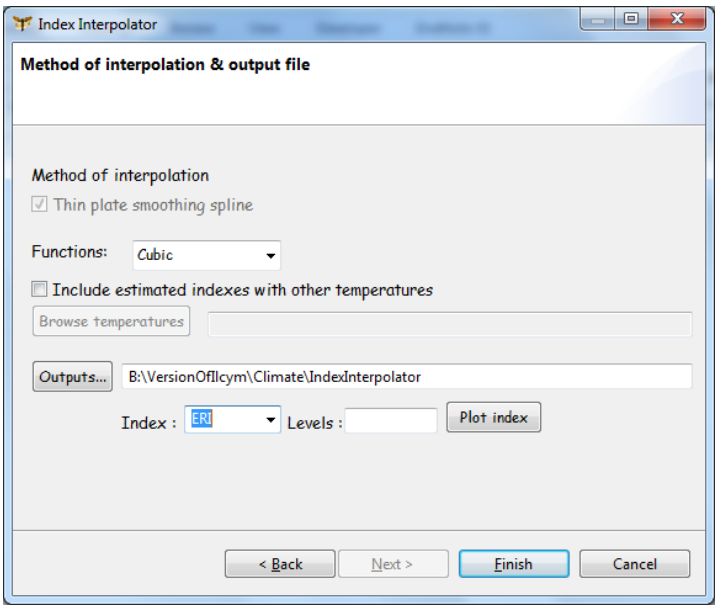


iii) Define the co variables for calculating the indices

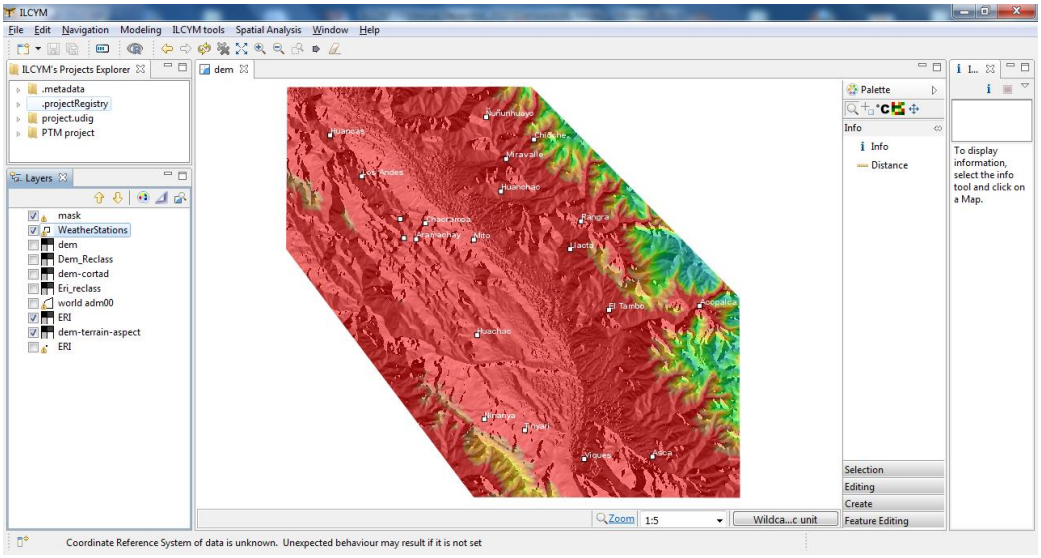


Note: It is mandatory to have the digital elevation model (*DEM*) as co-variables, latitude and longitude are optional.

iv) Define the function use by thin plate (cubic/quadratic)



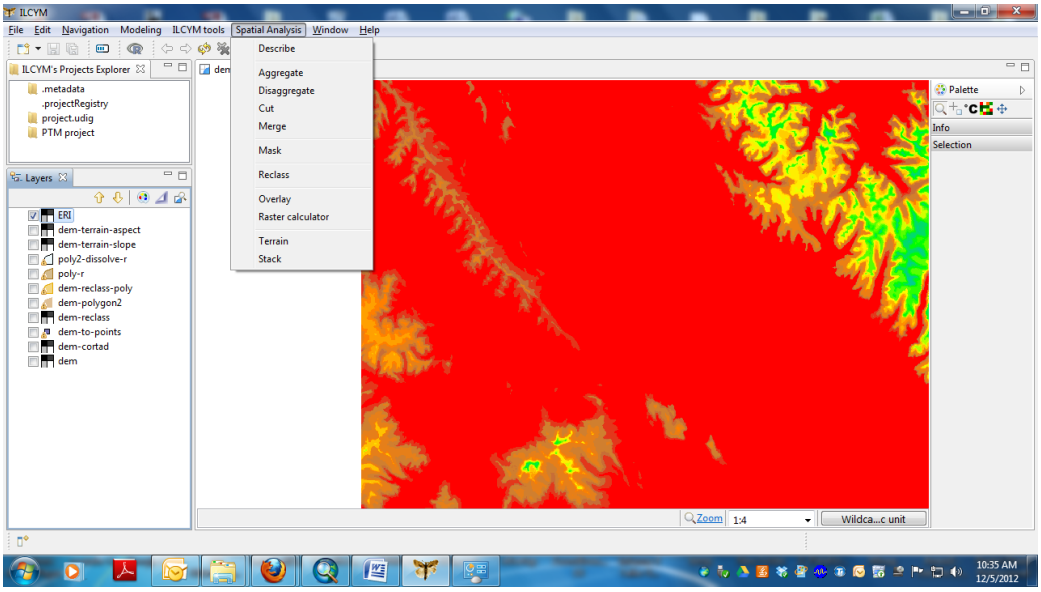
v) Outputs



3.3.3 Spatial Analysis

We used the Raster Package from R programming language to provide classes and functions for manipulating geographic (spatial) data in 'raster' format. Raster data divides space into cells (rectangles; pixels) of equal size (in units of the coordinate reference system). Such data are also referred to as 'grid' data. A number of practical and analytical functions are available from the menu ***Spatial Analysis***. The functions are particularly useful when using very large datasets that cannot be loaded into the computer's memory. Functions will work correctly, because they process large files in ***chunks***, i.e., they read, compute, and write blocks of data, without loading all values into computer memory at once.

The following window displays the overall features contained in the ILCYM-spatial analysis sub-module. To access these features, go to window, click on open perspective, select population analysis and mapping and click on spatial analysis.

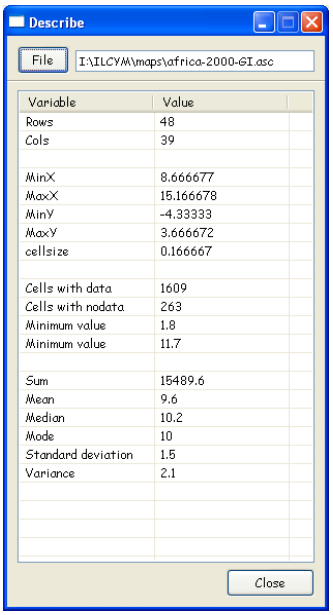


Below is a list of functions grouped by theme implemented in ILCYM.

Name	Description
Describe	Describes the content and structure of a grid file.
Mask	Cut a grid file as a template using a shape file.
Aggregate	Add cells in a grid file
Disaggregate	Disaggregated cells of a grid file.
Cut	Cut a section of a grid file.
Merge	Combines two Grid files into one file.
4Mask	Cut a grid file as a template using a shape file.
Reclass	Change the values of a grid file to create classes.
Overlay	Performs arithmetic on the values of the grid file resulting from two joint files.
Raster Calculator	For conducting algebra with grid files (addition, subtraction, multiplication, division, and additional math functions include log, square root, sine, etc.).
Terrain	For computing slope, aspect.
Stack	A stack is a set of raster with the same dimensions (number of columns and rows, and resolution) and location (minimum and maximum X and Y coordinates) which are handled together as a group

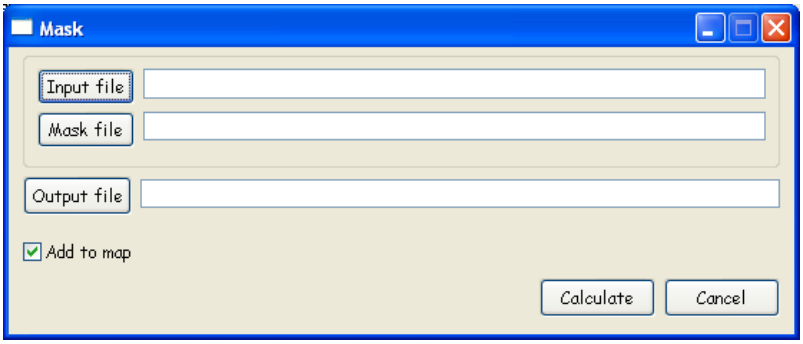
a) Describe window

Describe operates on the active layer when the window is open, or else on any layer selected using the "**Grid**" button. Some of the information (e.g., the number of rows and columns) can also be obtained by double-clicking on a grid layer in the legend (and choosing the "Info" tab). You can use this function to obtain the following information about the contents of a grid.



b) Mask window

Create a new Raster object where all cells that are ***NoData*** in a 'mask' object are set to ***NoData***, and that has the same values as x in the other cells. The mask can be either another Raster object of the same extent and resolution, or a Spatial object (e.g. Spatial Polygons) in which case all cells that are not covered by the spatial object are set to ***NoData***. This is frequently used when you wish to limit the output to match a specific shape of an existing grid.

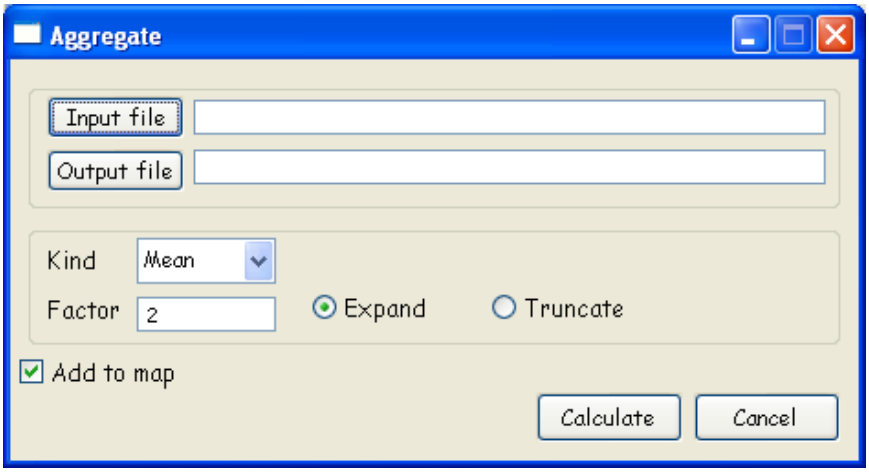


c) Aggregate

The aggregate tool is used to create a ***new Raster layer*** with a lower resolution. The Aggregate procedure allows indiscriminately grouping of cells in a grid file to an output file with a lower resolution (larger grid size). You must specify the aggregation factor which determines how many cells will be merged into one (and thus how big will the new cells). For example by a factor of 2, the new cells will have twice the length and two times the width of the original cell. In other words, four cells are merged into one.

Aggregation starts at the upper-left end of a raster. If a division of the number of columns or rows with factor does not return an integer, the extent of the resulting Raster object will either be somewhat smaller or somewhat larger than the original Raster Layer.

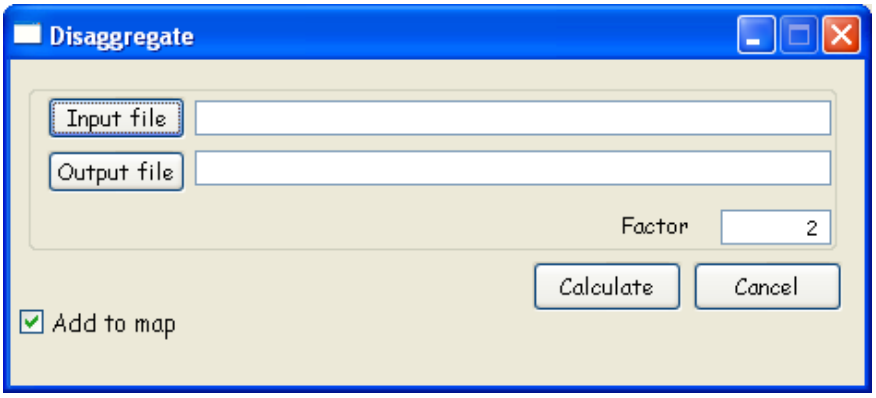
The values in the aggregate grid cells depend on the procedure chosen (maximum, mean, median, minimum, or sum fashion).



d) Disaggregate

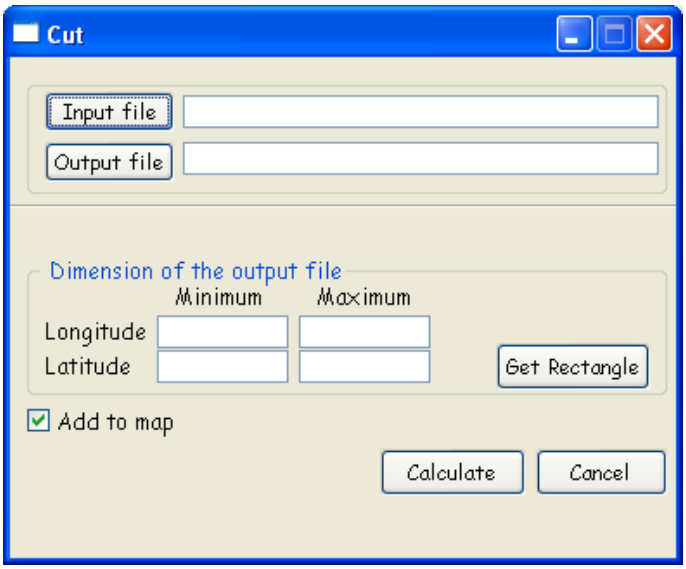
This feature is frequently used to create a new Raster layer with a higher resolution (smaller cells). The values in the new Raster Layer are the same as in the larger original cells. The tool divides the grid cells into smaller cells. The

values of the original cells are assigned to the smaller cells.



e) Cut

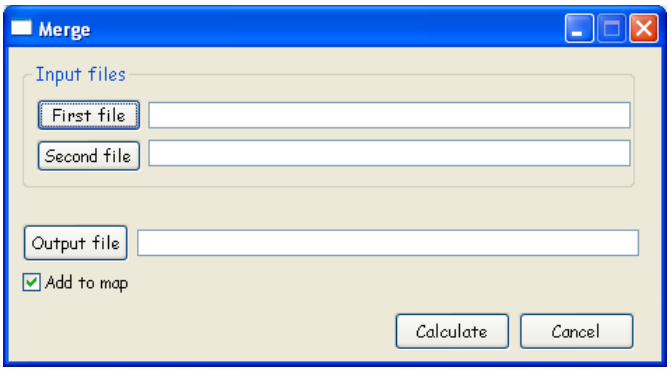
Cut allows you to make a new grid consisting of a selected part of the area of an existing grid. You can define the area to be cut and placed in the new grid by coordinates. These parameters can also be selected by drawing a rectangle on the map. They can also be copied from an existing grid.



f) Merge

The Merge function can be used to spatially append or mosaic Raster of different map extents; however, they must be in the same coordinate system. The Raster can be totally overlapping, partially overlapping, adjacent, or entirely separated. If the input Raster overlaps, the order of precedence is defined by the order of the raster in the argument list.

When the input Raster overlaps, it is viewed as a set of layers where ***NoData*** is transparent. The output Raster receives the first value at each cell that is not ***NoData***. For a set of overlapping raster, a number can be entered as valid input, but this input should be the last one in the list, since it will populate the remainder of the Raster.

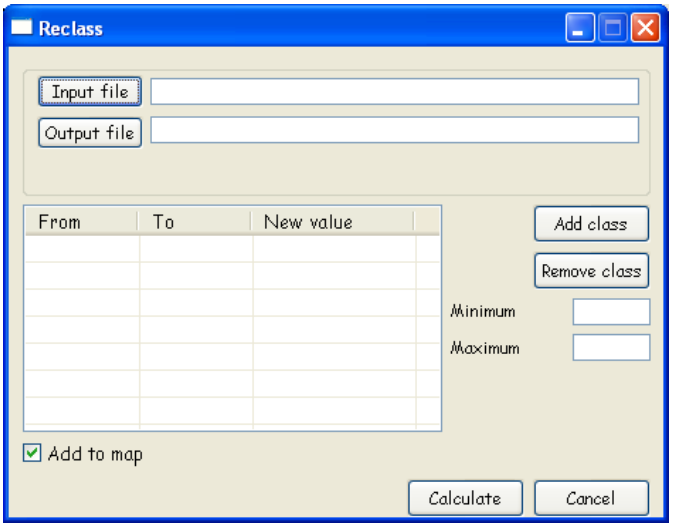


g) Reclass

Reclassifying your data means replacing input cell values with new output cell values. The most common reasons for reclassifying data are to

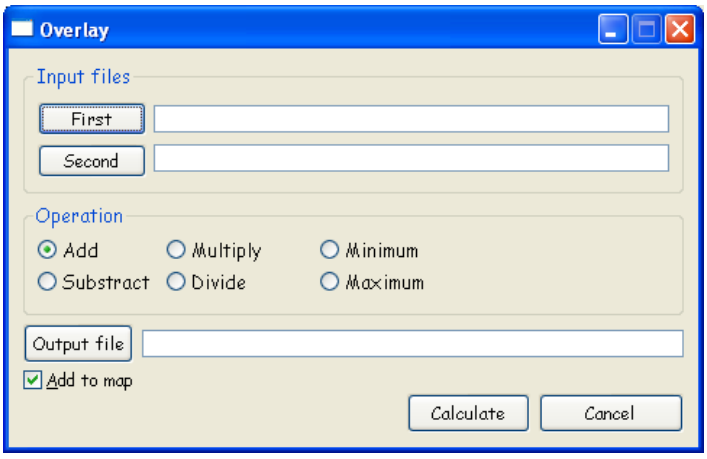
- Replace values based on new information.
- Group certain values together.
- Reclassify values to a common scale (for example, for use in a suitability analysis or for creating a cost raster for use in the Cost Distance function).
- Set specific values to ***NoData*** or to set ***NoData*** cells to a value

The function (re)classifies groups of values to other values. For example, all values between 1 and 10 become 1, and all values between 11 and 15 become 2. Reclassifies data from a grid according to class limits specified by the user. These limits can be adjusted manually. Add the button can be inserted extra classes, and with the Remove button these can be eliminated. ILCYM automatically displays the minimum and maximum file.



h) Overlay

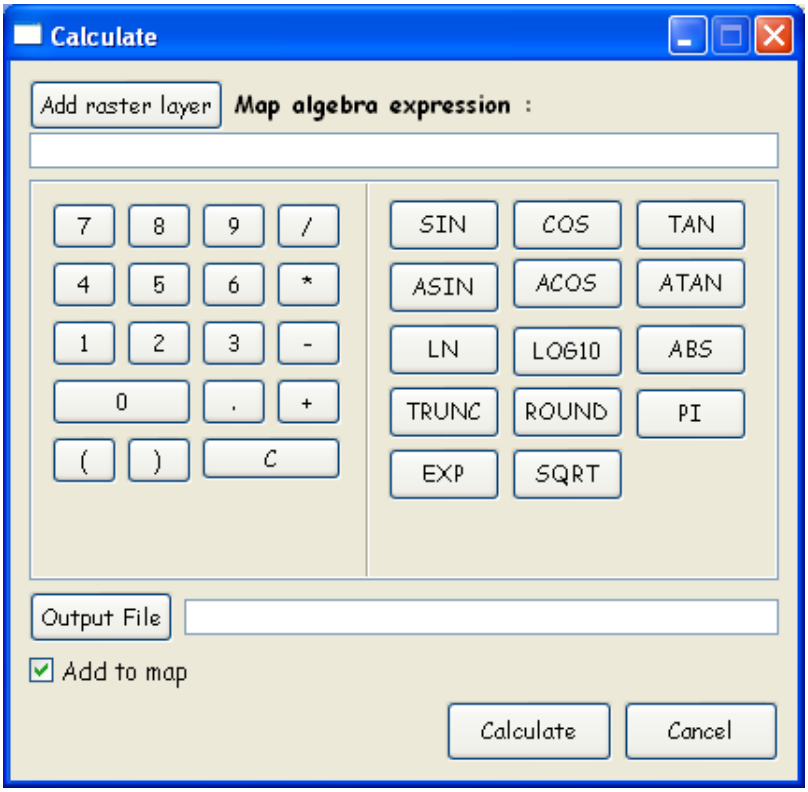
This tool is applied to two files with the same dimensions and location (number of columns and rows, resolution), and location (min and max X and Y coordinates). Overlay can stand one on the other (so to speak) and make some arithmetic operations on corresponding grid cells and place the results into a new file. Arithmetic operations covered include addition, subtraction, multiplication, division, and calculation of minimum and maximum values. Overlay allows you to place them on top of each other (as it were), carry out some arithmetic on corresponding grid cells (i.e., cells directly above each other), and place the results in a new, third grid. The arithmetical operations included are addition, subtraction, multiplication, division and calculation of minimum and maximum.



i) Raster Calculator

The Raster Calculator provides you a powerful tool for performing multiple tasks. You can perform mathematical calculations to create new map themes. In the Calculate window, you can do mathematical calculations with one or more grids. The advantage of Calculate is that you can do several steps at once. The disadvantage is that the calculations are much slower, so if you have very large grids you're better off using the Overlay function.

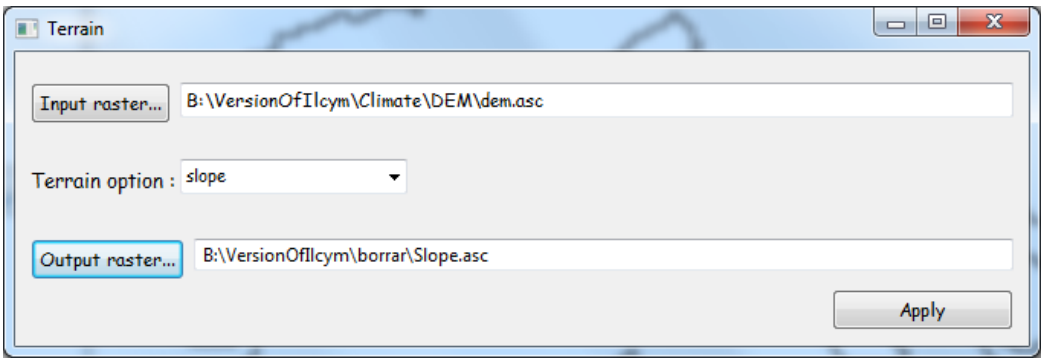
Use the "Add raster file" button to choose the files you want to use, insert the operator(s) you require between grid names, and provide a name for the output grid. As with Overlay, to be able to use Calculate with multiple grids, these must all have the same dimensions (number of columns and rows, and resolution) and location (min and max X and Y coordinates).



j) Terrain

This menu allows computation of slope, aspect characteristics from a raster with elevation data. The elevation data should be in map units (typically meter)

for projected (planar) raster data. They should be in meters when the coordinate reference system (CRS) is longitude/latitude.

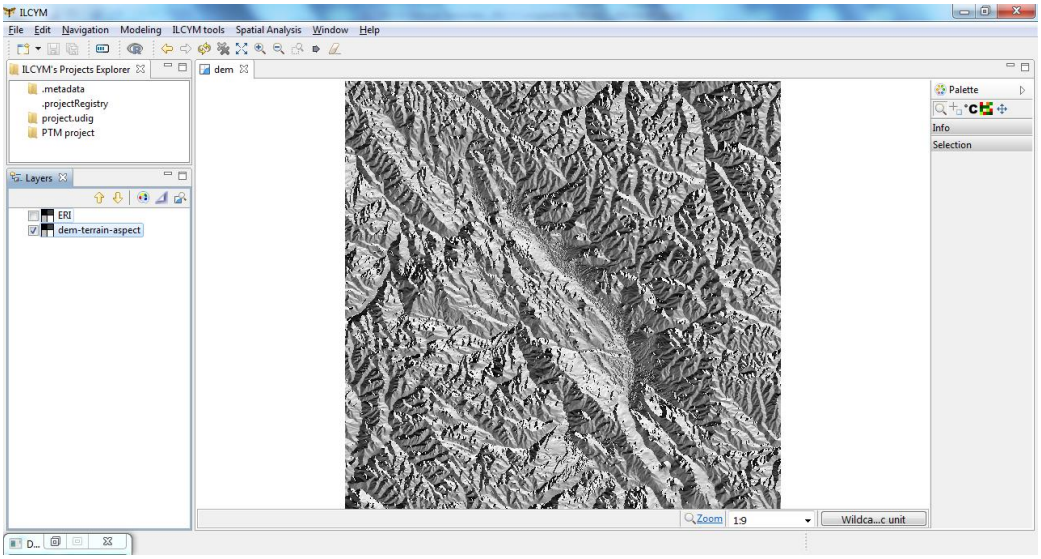


Aspect is measured in degrees (similar to a compass bearing) clockwise from magnetic north. A surface with 0 degrees aspect would represent a north direction, an east facing slope would be 90 degrees, a south facing slope would be 180 degrees and a west facing slope would be 270 degrees.

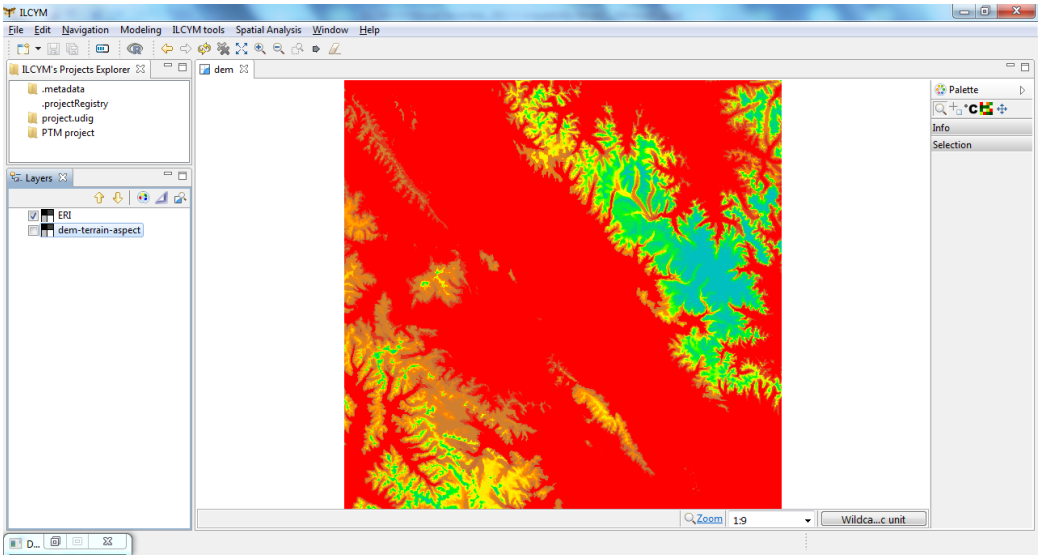
The aspect identifies the downslope direction of the maximum rate of change in value from each cell to its neighbors. Aspect can be thought of as the slope direction. The values of the output raster will be the compass direction of the aspect.

The slope identifies the gradient, or rate of maximum change in z-value from each cell of a raster surface.

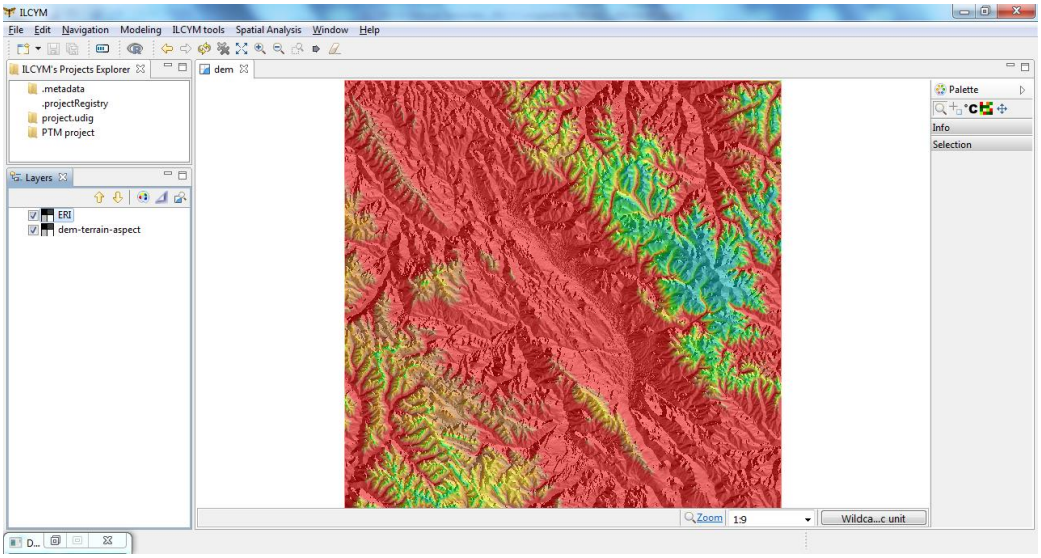
i) Displaying terrain faces by aspect



ii) Index map



iii) Displaying terrain faces by aspect combined with index map (it help to visualize the index in 3d)



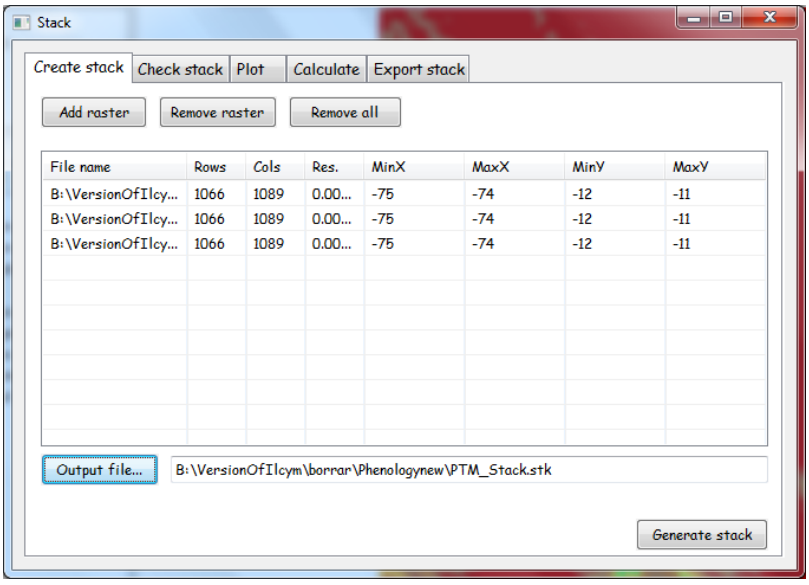
k) The Stack menu

A stack is a set of raster with the same dimensions (number of columns and rows, and resolution) and location (minimum and maximum X and Y coordinates) which are handled together as a group. Grouping rasters in a stack makes it easier to process many files in the same way, and allows a number of additional analytical procedures.

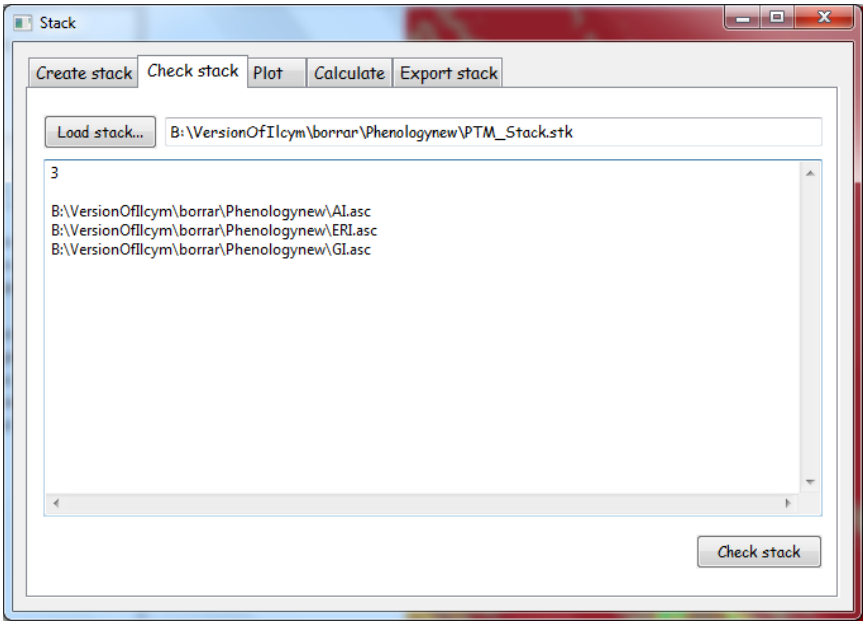
A stack is stored in a file with the extension STK. A STK file is nothing but a list of the grids that the stack contains. It does not contain any of the actual data in the grids. Rather, it points to the existing files with the data. Therefore, if you delete, rename, or move one its constituent grids to a different directory, the stack will become invalid.

You can make a stack by adding ASCII files to a list and then naming the output STK file. You can remove raster from the list individually or all at once if you make a mistake or change your mind. ILCYM tells you about the dimensions and location of each grid you add to the stack. These must be identical for all grids in the stack.

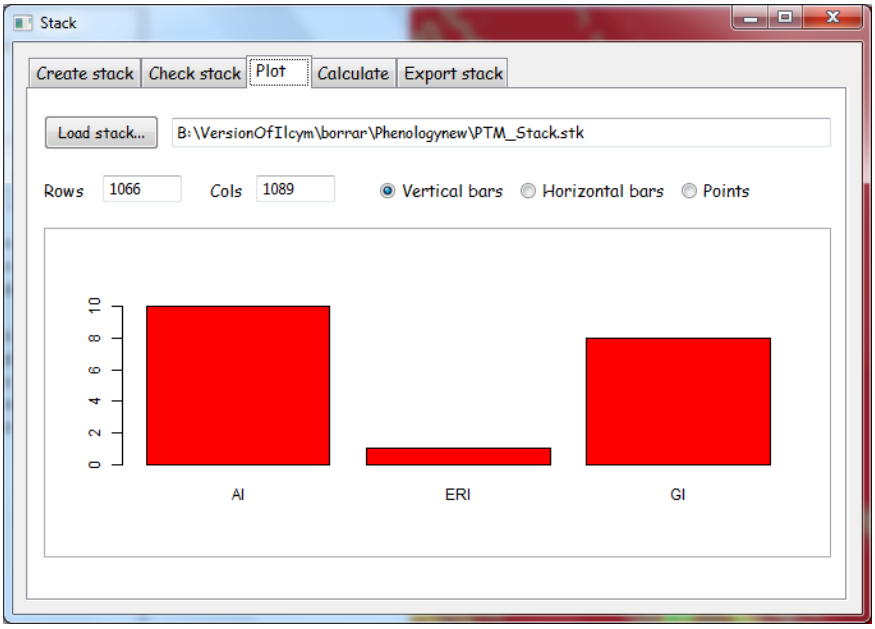
i) Add raster to the stack



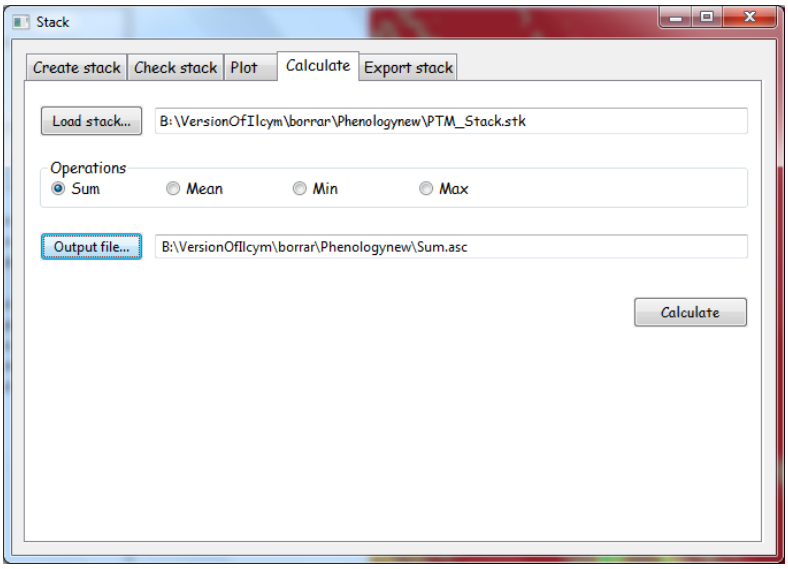
ii) If you forget which grids are in a stack, or wonder whether it is still valid, use the Check Stack tab to obtain a list of the grids included in a specified stack.



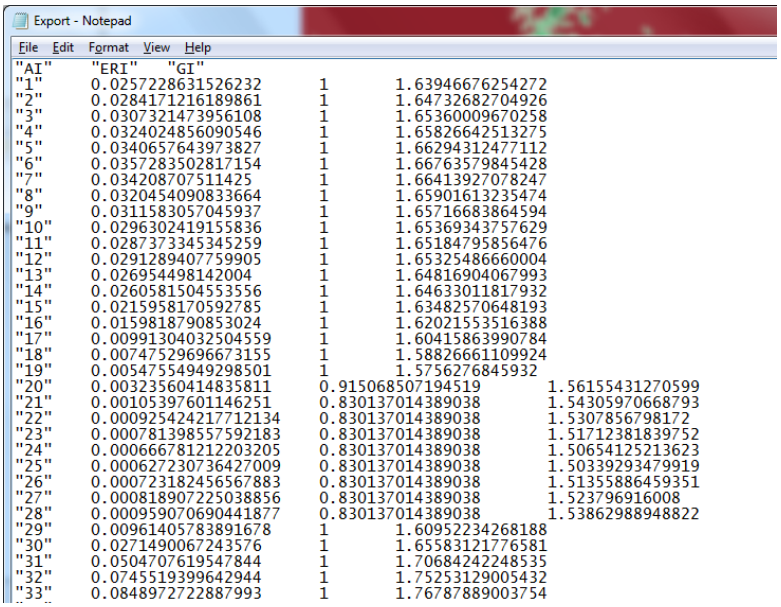
iii) You can plot and make a histogram of the values of corresponding cells in all Ascii in a stack.



iv) Using Calculate, you can produce a single raster from the multiple rasters in a specified stack, the value in each cell of the output grid being the sum, mean, minimum, or maximum of the values rasters in the stack.



v) Finally you can Export the all the raster files in the stack together to a single TXT file. Such a file can be used to make comparisons on a cell-by-cell basis, e.g. in a spreadsheet program.



3.3.4 Managing layers

a) Navigation Tools

The Navigation Menu allows you to control what the current Map editor is displaying.

Zoom Tool. The Zoom tool allows the user to zoom towards or away from the map.

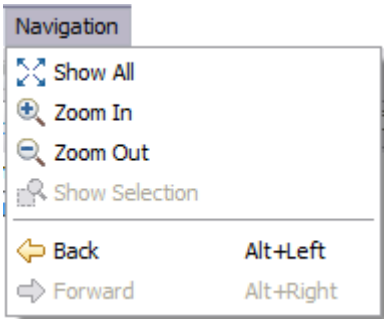
The Zoom tool provides the following options:

- If the left mouse button is clicked then the zoom is towards the map. The point clicked is the new center of the display after the zoom.
- If the right mouse button is clicked then the zoom is away from the map. The point clicked is the new center of the display after the zoom.
- If the left mouse button is dragged to form a box then the box indicates the new area that will be displayed on the screen (a zoom in).
- If the right mouse button is dragged to form a box then the area on the screen during the drag will be fit into the box (a zoom out).
- Rotating the mouse wheel will zoom towards or away from the map, keeping the center of the display the same.

An alternative to using the mouse wheel is holding alt- and moving the mouse left or right.

Pan Tool. A drag with the left mouse button down will move the map across the display.

Navigation Commands: May of these commands may also be found in the Navigation Menu.

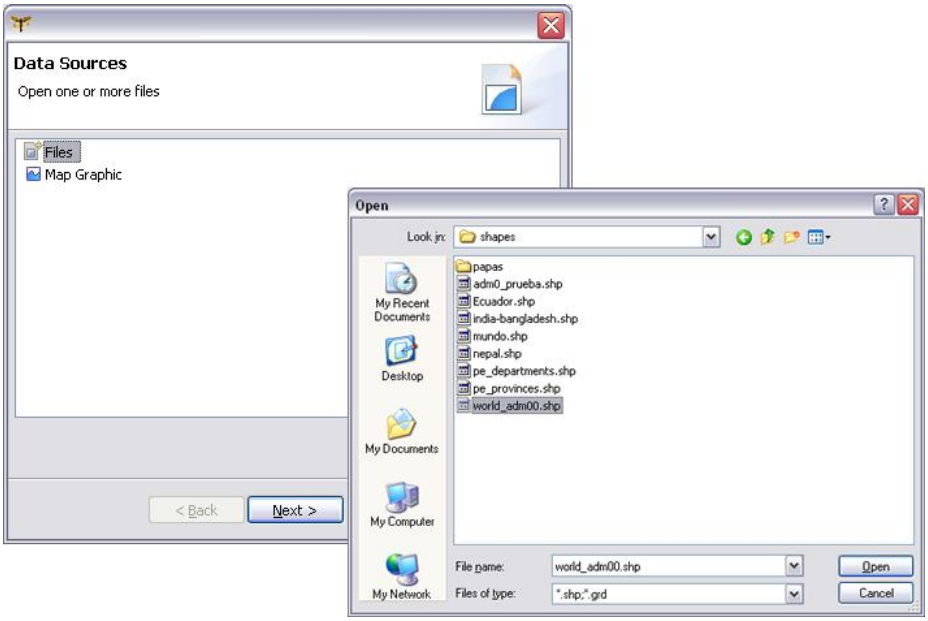


- **Back:** Displays the previous view. The back button is active only after the view has been changed and is not saved between sessions.

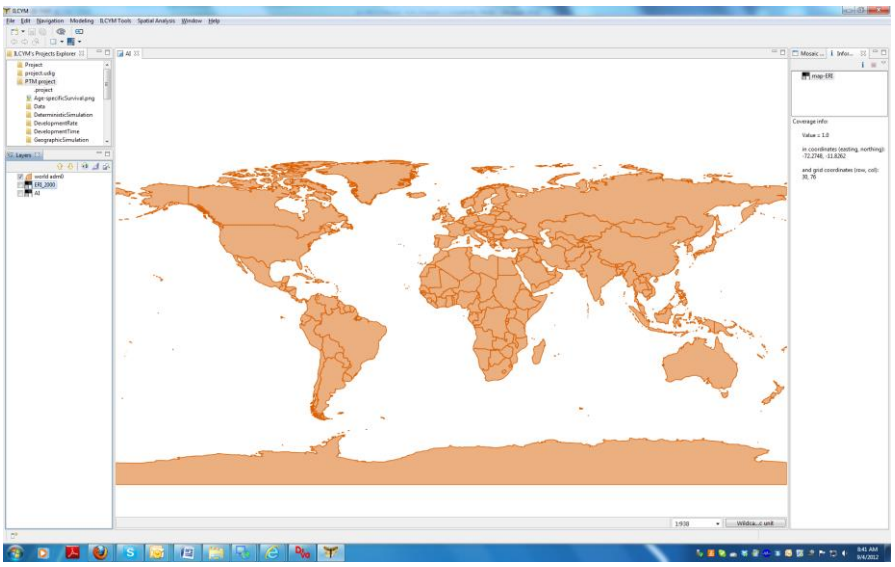
- ***Forward:*** Displays the next view. The forward button is active only after the back button has been pressed.
- ***Refresh:*** Redraw the screen.
- ***Stop Drawing:*** Stop the current rendering process.
- ***Show All:*** Sets the zoom so that all available data is displayed.
- ***Zoom-In:*** The Zoom-In button zooms towards the data by a set amount. The center of the zoom is the center of the map.
- ***Zoom-Out***: The Zoom-Out button zooms away from the data by a set amount. The center of the zoom is the center of the map.
- ***Zoom to Selection***: Zoom to the selected features

b) Add shape file wizard

This wizard helps you import spatial data and add it to a Map. When the Add Data Wizard first comes up you must choose data source to work with.
Some simulations may request a map to be loaded in the software, to load one or more maps go to *File* **File** -> ***New***-> ***New Layer*** **option** or **click in the next button** and the next window will appear. This is useful to have a reference in the map where to Start Spatial simulation.

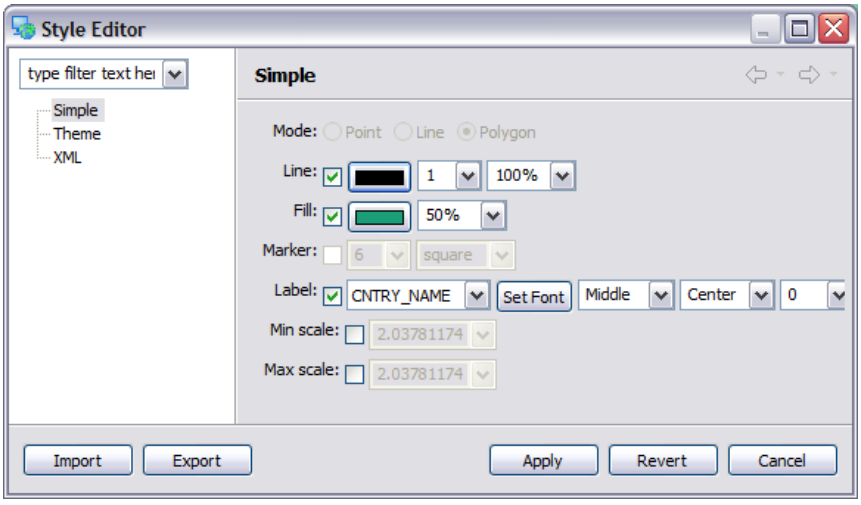


Click on ***File*** and then ***Next*** and look for the path of one shape, p.e. world shape.



c) Style Editor dialog

The style editor dialog is used to modify layer's display on screen.



A tree of style pages for the selected content is displayed. Each page allowing the modification of one aspect of the visualization process.

Apply: Press this button to update the Map with the current settings.

Revert: Reset the style pages to their previous settings.

Close: Dismiss the style editor.

Import: Import style settings from an sld file.

Export: Export style settings to an sld file.

Feature Style Pages

When the Style Editor dialog is opened on a feature layer the following pages are available.

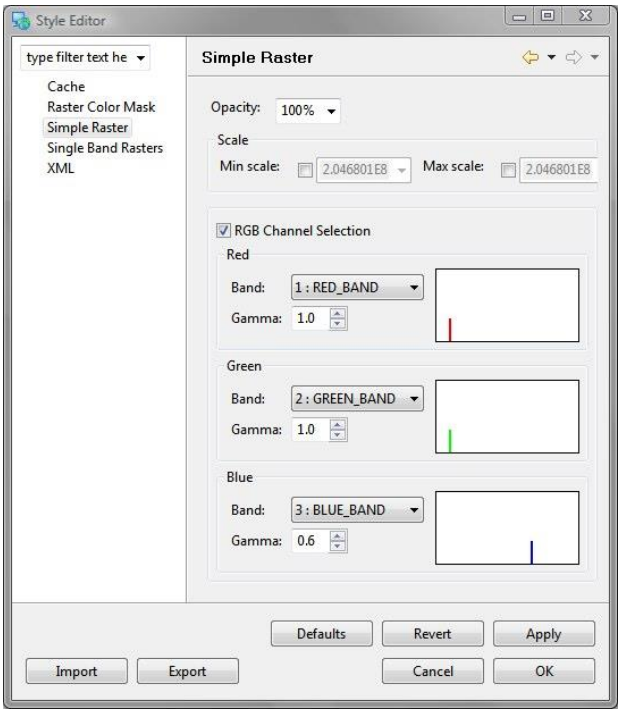
- Cache
- Filter
- Simple Feature
- Simple Lines
- Simple Points
- Simple Polygons
- Theme
- XML

Raster Style Pages

When the Style Editor dialog is opened on a raster layer the following pages are available.

- Raster Color Mask: The Raster Color Mask makes a single color of a coverage transparent. Often used in satellite images to indicate areas where no information was recorded.

- Simple Raster: Allows simple control over the rendering of a raster image.



Opacity: allows the transparency of an image to be set; often useful to allow artificial boundaries to show through the raster.

Scale: Control the scale at which the raster is shown

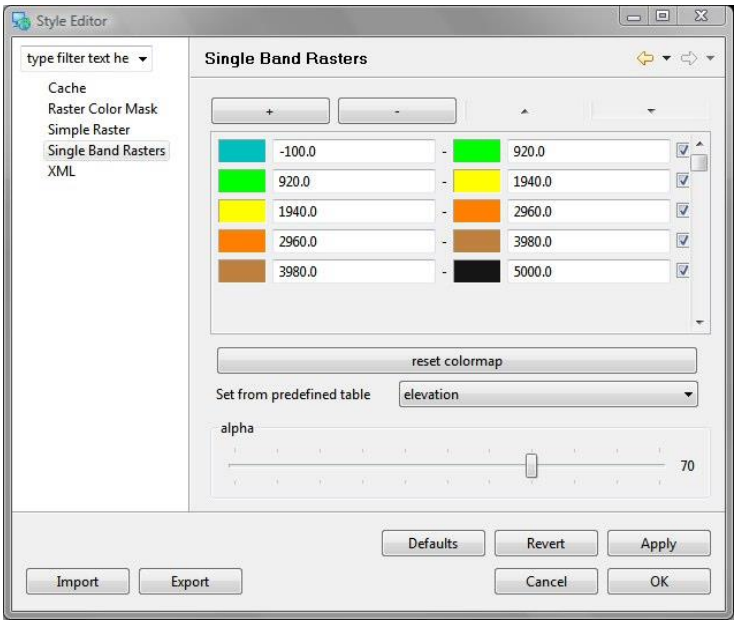
RGB Channel Selection: Provides control over mapping raster channels to Red, Green and Blue channels for display. The gamma of each band can be controlled allowing you to adjust how much of a contribution each band makes to the final display.

Band: Allow the selection of a data band. Most processed images are already defied in terms of Red, Green and Blue. If you are working with raw satellite information you will need to carefully select the correct radar, visual light or infrared band for the analysis being performed.

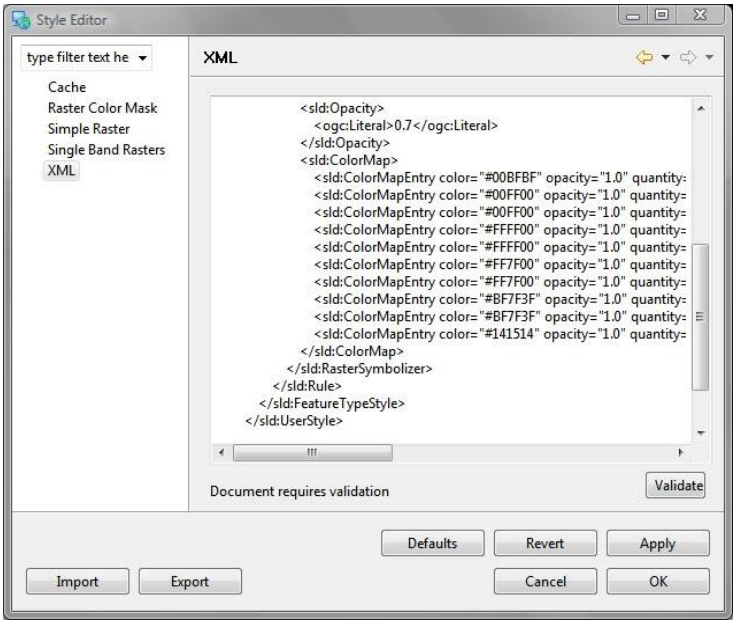
Gamma: Allows fine grain control over the contribution being made.

0-1: Multiplies the contribution; brightening the channel accordingly, 1.0: Direct 1 to 1 ratio, 1-*: Minimises the contribution; dimming the channel accordingly

- ***Single Band Rasters:*** Used to handle single band rasters (such as digital elevation models) where you can map value ranges to artificial colours for display. A number of predefined color maps are provided.



- ***XML:*** This page is used to allow raw access to the xml used to express style information. The XML format used is the Stlye Layer Descritor specification by the Open Geopspatial Consortium.



Validate: Press this button to check that your XML is valid.

3.3.5 Spatial simulations and mapping

a) Estimating life table population parameters

ILCYM simultaneously extracts for a selected region the daily or monthly maximum and minimum temperature data for one year (365 days or 12 months data sets) with their respective geographical coordinates from the database. The extracted temperature data are organized in either in 365x2 (for daily data) or 12x2 (for monthly) matrices using the longitude as column and latitude as rows representing 365 or 12 matrices each for the minimum and maximum temperatures. Thereafter, a point object is created for each geographical coordinate (longitude and latitude) in the form of a table with two columns (the first column includes the minimum temperatures and the second the maximum temperatures that is directly used for spatial phenological simulation. With these temperatures and the phenology model of the species, the generation length, the net reproduction rate, the intrinsic rate of population increase, the finite rate of increase and the doubling time are estimated (Kroschel *et al*. 2013).

Temperature inclusion in the phenology model

Using cosines approximation of temperature, the indices can be mapped under present and projected SRES emission scenarios for predicting responses to present and future climates.

Calculation of Indices

From life table parameters, formulations yielding to three indices are conducted (Kroschel *et al*. 2013).

i) Establishment (survival) index (*ERI*)

The establishment risk maps visualize the capacity of invasive pest species to establish permanent populations based on spatial and temporal variability in temperature. They assist identifying the regions where a species has the potential to pose an invasive threat after the pest's introduction.

The map plots an index (establishment risk index, ERI), which is the ratio between periods (time intervals) in which population are expected to increase and total periods within a year. The index is defined as the number of time

intervals with a net reproduction rate, R0, above 1 (I_i=1) divided by the total number of time intervals within a year (I_I). By default the maps, as presented in the atlas, are generated by using a 1-month time scale; however, the calculation can be also based on other time scales (for example, 1-day intervals). The formula for using monthly intervals is as follows:

$$ERI = \frac{\sum_1^{i=12,} I_i}{I_I}$$

in which I_i is the interval of the month i (with i = 1, 2, 3,…, 12) and its value is 1 if the population is expected to increase within this interval (I_i = 1 if R0 ≥ 1) and the value is 0 if the population is expected to decrease (I_i = 0 if R0 < 1) according to the established temperature-driven phenology model, and the total number of intervals, I_I, is 12.

If the index is calculated on a daily time scale the formula becomes:

$$ERI = \frac{\sum_1^{i=365,} I_i}{I_I}$$

where I_i than is the interval of day i (with i = 1, 2, 3,…, 365) and the total number of intervals, I_I, becomes 365.

The ERI takes values between 0 and 1. A ERI=1 represents areas where the specie's population is expected to grow throughout the year. An ERI<1 characterizes areas in which population growth is restricted to certain periods of the year; for example, an ERI=0.25 indicates an area where populations are expected to grow only during 3 month (3/12) of the year and decrease during the other 9 month (9/12).

If the index is used for a prospective antagonist species (p.e. parasitoids) considered for release as a non-native biological control agent, the index expresses the capacity or potential to establish in an area that might be considered for inundative or inoculative release of the species. In these cases, the index represents the establishment potential of the species, which is desired for long-term control of the target pest species.

Generally, by default, the maps are generated using a monthly time scale that is adequate for multivoltine species; these species have generally a short generation time with overlapping generations. However, such a short time interval is not appropriate for univoltine species, which produce a single generation within a year, because single life stages only develop during certain periods of the year. Hence life table parameters, like the net reproduction rate, calculated for a given period are not representative for the species population development. For estimating the establishment risk of univoltine species, the whole life cycle of the pest need to be simulated throughout the year (at best for several years with real temperature records as input data) using ILCYM's

“deterministic simulation” tool. If the population increases during a year the establishment risk can be considered high.

It should be also noted that the index is based on data and information describing the temperature-dependent phenology of the species and the temperature variability observed within a restricted area (generally, the simulation is based on temperature interpolated from historical data). Therefore, the index does not indicate the risk of introduction, which depends on many other factors (potential pathways of introduction). Effects of other biotic or abiotic factors that might depress pest populations are not included in the calculation; for example the availability of host species. The latter can be addressed by simulating the index only for areas in which pest-specific host plants are produced (i.e. by using the area of production as a filter in GIS modeling, as applied in the potato pest atlas). For pest antagonists, similarly, areas can be filtered by using only areas where the target pest prevails today

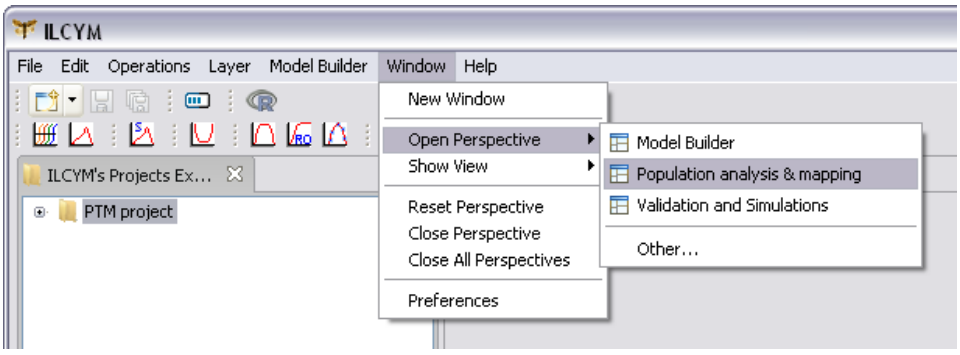
ii) Generation index (*GI*)

The generation index estimates the mean number of generations that may be produced within a given year. The index is computed by averaging the sum of estimated generation lengths, calculated for each Julian day.

iii) Activity index (*AI*)

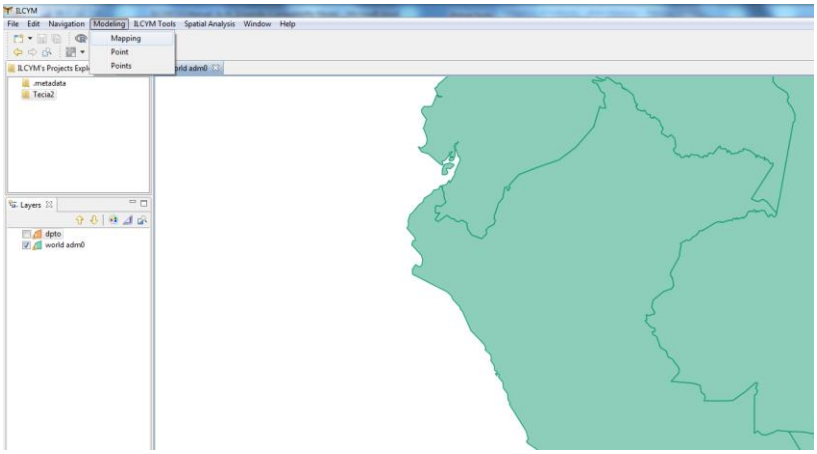
This index is explicitly related to the finite rate of population increase, which takes the whole life history of the pest into consideration; for example, an index value of 4 would illustrate a potential population increase by a factor of 10,000 within one year (all other population limiting factors, including food availability, etc., are neglected).

To access the Population analysis and mapping perspective, go to **menu Window** -> **Open Perspective** and **Select** Population analysis & mapping.

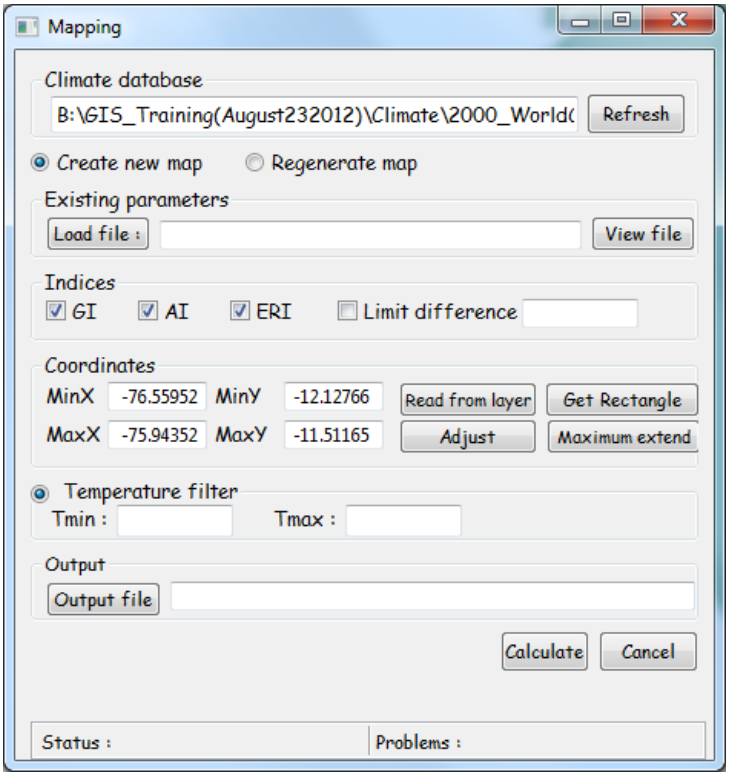


b) Mapping phenology model

Go to ***Modeling menu*** -> ***Mapping***.

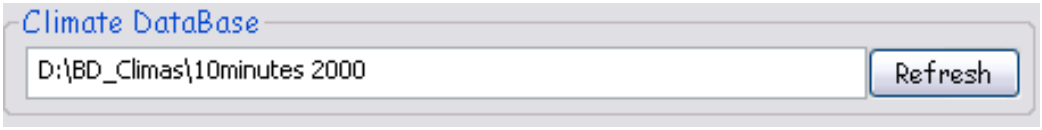


This window below will appearfor geographic simulation

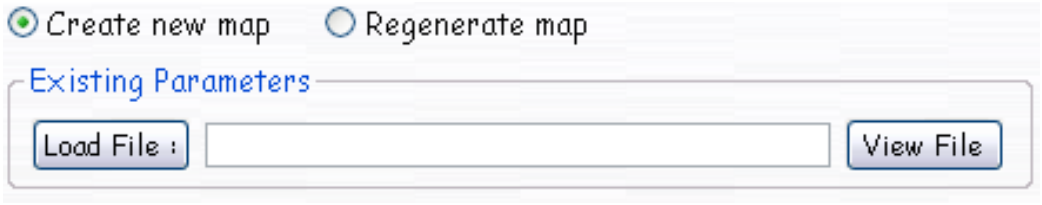


The climate database tool is for viewing and refreshing the climate data base path. When a data base is change (i.e replacing 10 minutes 2000 to 10 minutes

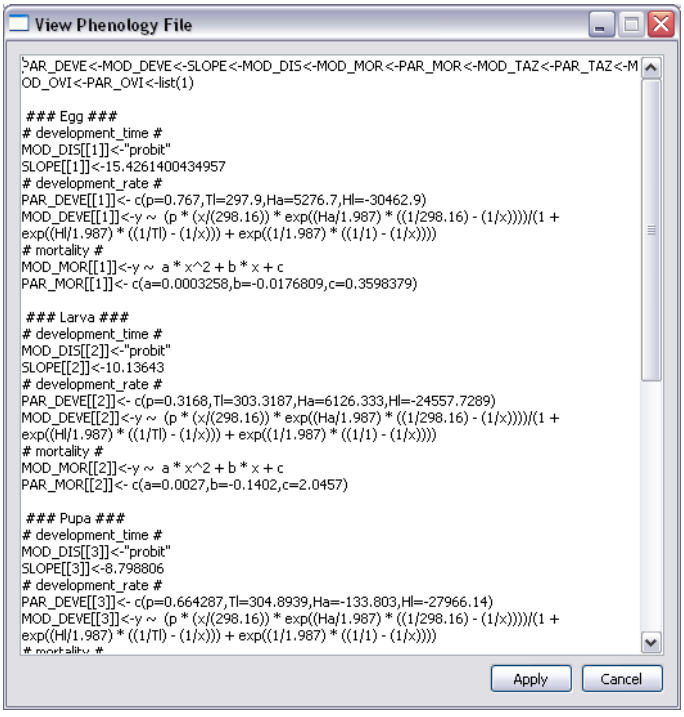
2050), the user utilizes this tool for updating the path in the geographic simulation window after reloading a new data base.



This tool allows creating a new map or creating more maps from an existing phenology

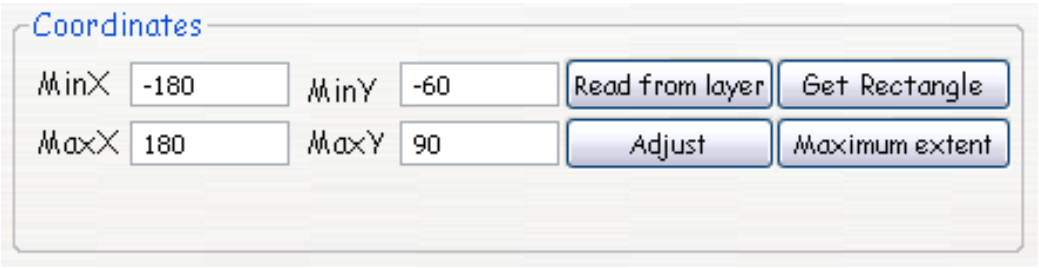


- ***Create new map* option:** create a new map.
- ***Regenerate map* option:** create a map with an existing phenology.
- ***Load file* button:** load the existing phenology file, this button is enabled when *Regenerate map* is selected.
- ***View file* button:** open the existing phenology to verify the intensity or for possible modification, this button in enabled when *Regenerate map* is selected.


View Phenology File
PAR_DEVE<-MOD_DEVE<-SLOPE<-MOD_DIS<-MOD_MOR<-PAR_MOR<-MOD_TAZ<-PAR_TAZ<-MOD_OVI<-PAR_OVI<-list(1)
Egg
# development_time #
MOD_DIS[[1]]<-"probit"
SLOPE[[1]]<-15.4261400434957
# development_rate #
PAR_DEVE[[1]]<- c(p=0.767,Tl=297.9,Ha=5276.7,Hl=-30462.9)
MOD_DEVE[[1]]<-y ~ (p * (x/(298.16)) * exp((Ha/1.987) * ((1/298.16) - (1/x))))/(1 + exp((Hl/1.987) * ((1/Tl) - (1/x))) + exp((1/1.987) * ((1/1) - (1/x))))
# mortality #
MOD_MOR[[1]]<-y ~ a * x^2 + b * x + c
PAR_MOR[[1]]<- c(a=0.0003258,b=-0.0176809,c=0.3598379)
Larva
# development_time #
MOD_DIS[[2]]<-"probit"
SLOPE[[2]]<-10.13643
# development_rate #
PAR_DEVE[[2]]<- c(p=0.3168,Tl=303.3187,Ha=6126.333,Hl=-24557.7289)
MOD_DEVE[[2]]<-y ~ (p * (x/(298.16)) * exp((Ha/1.987) * ((1/298.16) - (1/x))))/(1 + exp((Hl/1.987) * ((1/Tl) - (1/x))) + exp((1/1.987) * ((1/1) - (1/x))))
# mortality #
MOD_MOR[[2]]<-y ~ a * x^2 + b * x + c
PAR_MOR[[2]]<- c(a=0.0027,b=-0.1402,c=2.0457)
Pupa
# development_time #
MOD_DIS[[3]]<-"probit"
SLOPE[[3]]<-8.798806
# development_rate #
PAR_DEVE[[3]]<- c(p=0.664287,Tl=304.8939,Ha=-133.803,Hl=-27966.14)
MOD_DEVE[[3]]<-y ~ (p * (x/(298.16)) * exp((Ha/1.987) * ((1/298.16) - (1/x))))/(1 + exp((Hl/1.987) * ((1/Tl) - (1/x))) + exp((1/1.987) * ((1/1) - (1/x))))
Apply
Cancel

Select one or more checks of the indices.

Input the geographic coordinates of the region to simulate.



***Read from layer* button:** read the coordinates of the layer selected.

***Adjust* button**: adjusts the coordinates to the closer point, taking the database as reference

Get Rectangle* button:** automatically generated the coordinates of the selected area by clicking in the ILCYM box Selection tool located in the toolbar*** .

***Maximum extent* button:** get the coordinates of data base.

Temperature filter (optional): this option allows the user to filter temperatures in the climate database, and the user is required to enter the lower and upper limits of temperatures (range of temperature that your species are adapted to), this will speed-up the process of estimating indices and will only produced values within your chosen range. Such option may guide the user to not estimate indices on zone of extreme temperature like the desert or pole.

Select the path and name of the output map.

Clicking on Apply button*:* the simulation will run, this process take some minutes or hours depending on the size of area and the resolution.

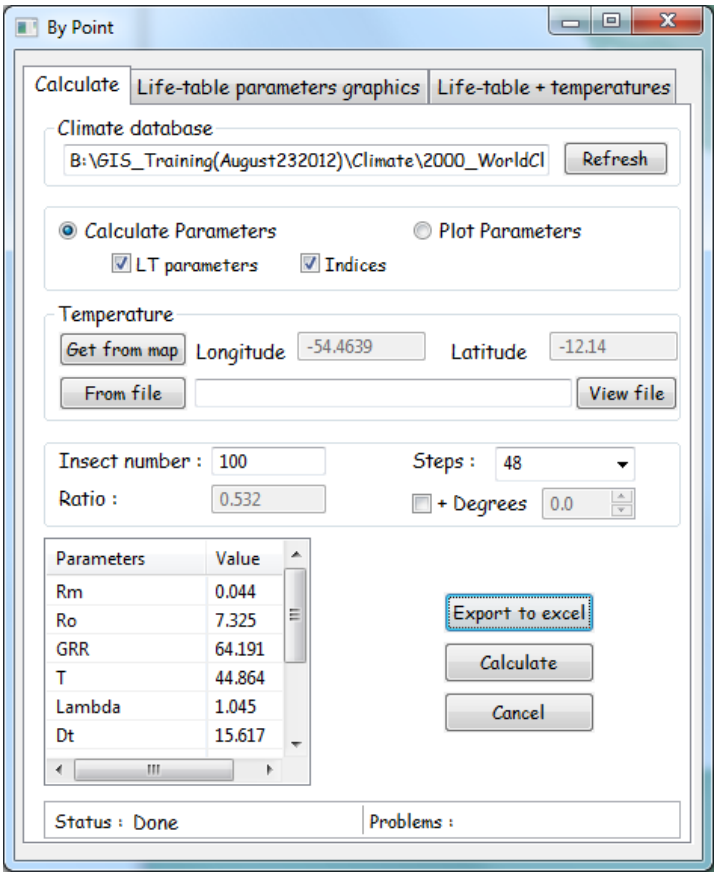
Summary on how to create a map in ILCYM

- Load climate data base,
- Add shape file,
- Select the project,

- Go to geographic simulation,
- Select the region to simulation by clicking on the ILCYM box selection tool
- Click on get rectangle,
- Designate or write the name of the output file,
- Click on apply button and wait for several minutes or hours or days, depending on the size and resolution of the maps,
- Load the map (the steps are identical to ***adding shape file***)

c) Simulation Point

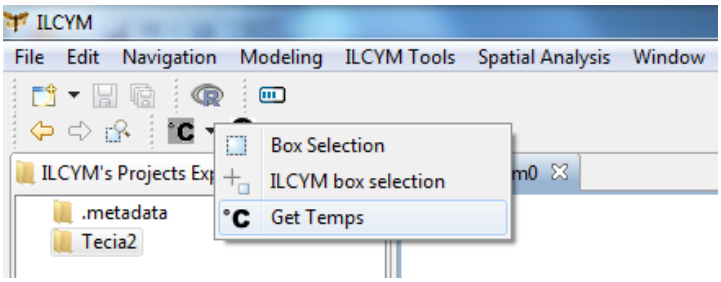
Under ILCYM ***population analysis and mapping perspective*** menu go to Modeling and ***click*** on ***point***. The following window will appear where you can simulate the life-table parameters and/or indices in a location. Also the user can upload its own temperature data file to calculate these indices.

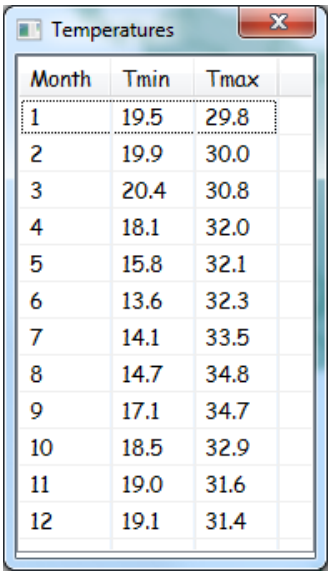


With **Calculate** we estimate the life table parameters and the indices, with **Life-table parameter graphics** you visualize them, and with **Life-table +**

temperatures you visualize the life table and the corresponding input temperature.

- ***Climate database - refresh:*** This is for actualizing the climate database by clicking on ***refresh***.
- ***Calculate parameters:*** Option for calculating life table parameters. ***Parameters* check:** calculates only the life-table parameters. ***Indices* check:** calculates only the indices.
- ***Plot parameters:*** Option for plotting life table parameters.
- ***Get from map*:** Allows you to obtain the temperatures values of the point in the map by clicking in the ***Get temps* button** located in the toolbar, then clicking on the map the location you want, and finally clicking on the ***Get from map* button** from ***By point window***.
- ***Longitude* text box:** is automatically filled when the user select one point of the map.
- ***Latitude* text box:** is automatically filled when the user select one point of the map.

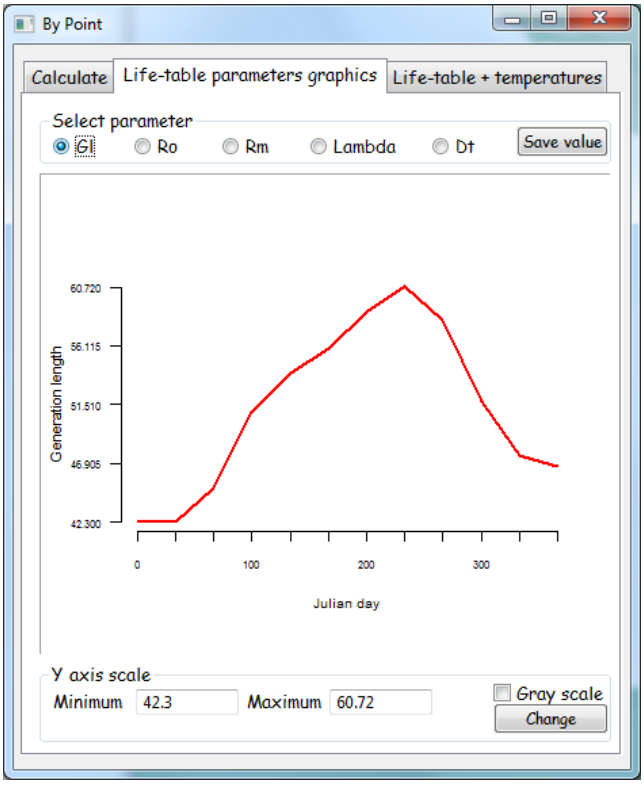




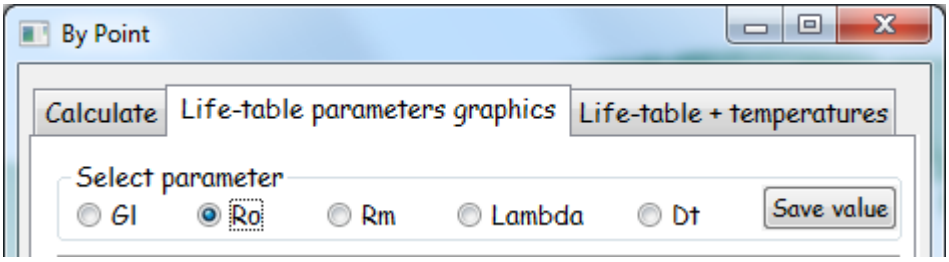
Month	Tmin	Tmax
1	19.5	29.8
2	19.9	30.0
3	20.4	30.8
4	18.1	32.0
5	15.8	32.1
6	13.6	32.3
7	14.1	33.5
8	14.7	34.8
9	17.1	34.7
10	18.5	32.9
11	19.0	31.6
12	19.1	31.4

- ***Get from file – view:*** Allows you to upload temperatures values from a file and the view button allows you to view the value.
- ***Insect number:*** number of insects.
- ***Steps combo:*** time step for your simulation which is the multiple of 4 which represents de number of hours within a day. For example choosing 48 means your time steps is half an hour.
- ***Ratio* text box:** ratio between females and males appears automatically from your phenology model.
- ***Degrees text box*:** for analyzing the effect of temperature increase.
- ***Calculate:*** allow the calculation.
- ***Export to Excel:*** for exporting the output to an excel file.

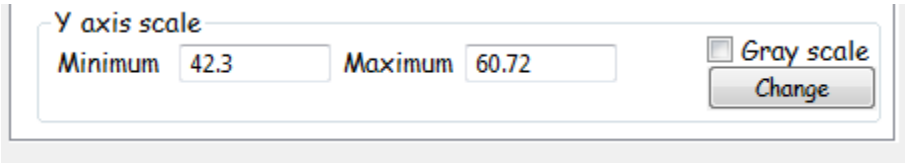
By selecting **Get parameters option** we can calculate the life-table parameters and the indices. If the user select ***Get graphics option*** this image will appear showing the variation of the parameter in the year.



Select each life-table parameter to plot its variation in the year



- ***Save value* button**, this button saves the value of the parameter.

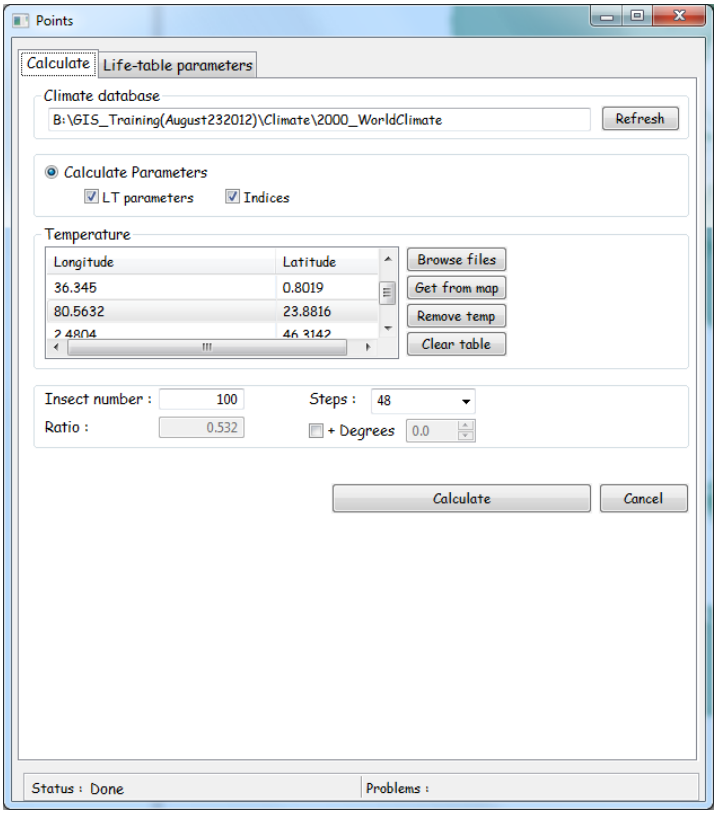


- ***Change*:** modify the Y axis scale.
- ***Gray scale* check:** displays the graph in gray scale

ILCYM can jointly display the parameters variation with temperature for a year.

d) Simulation Points

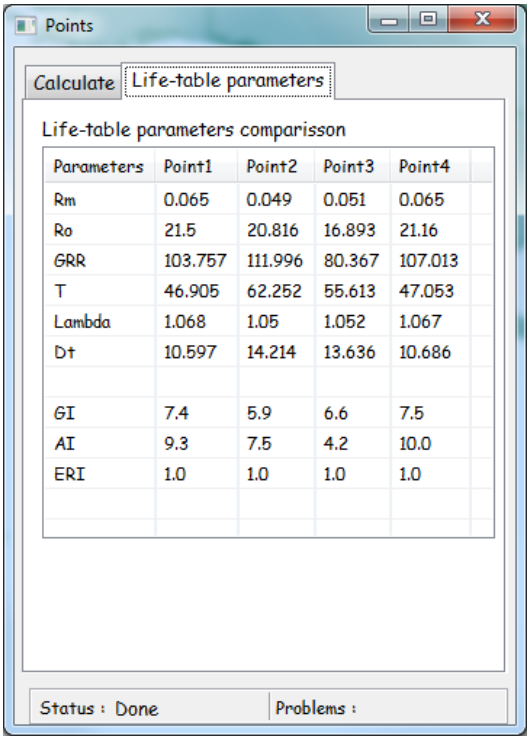
Under ILCYM population analysis and mapping perspective menu go to Modeling and click on points. The following window will appear where you can simulate the life-table parameters and/or indices in several locations (maximum 4).

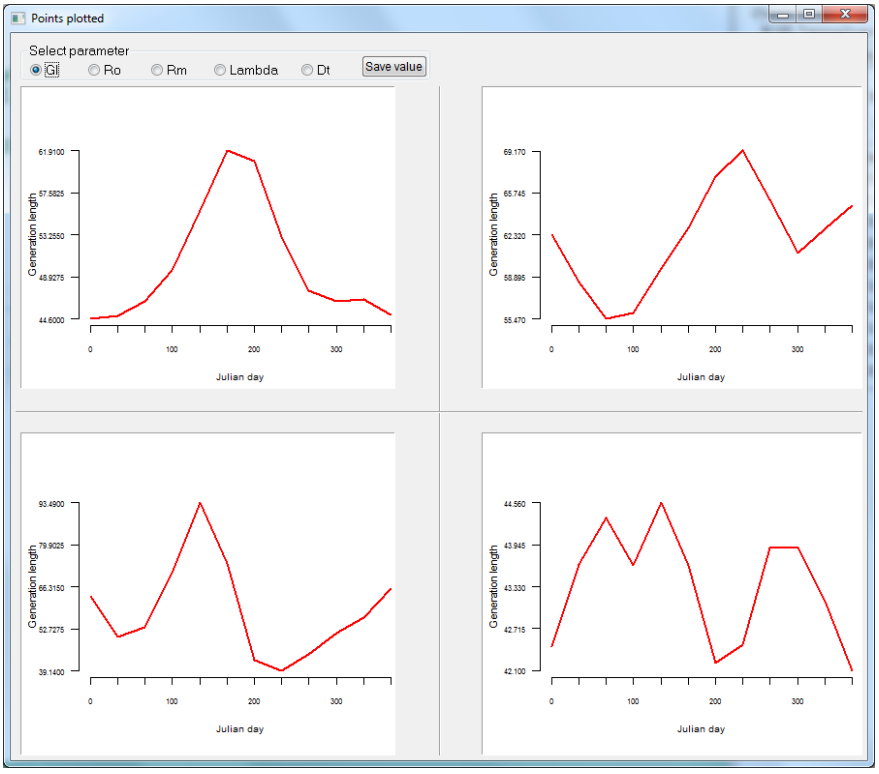


The button on the window above has similar meaning as on **point analysis window**.

- ***Remove temp*:** Allow you to remove a longitude & latitude from selections.
- ***Clear table*:** Allow you to clear all selections.

After calculating with **Calculate option** we will obtain the windows below.





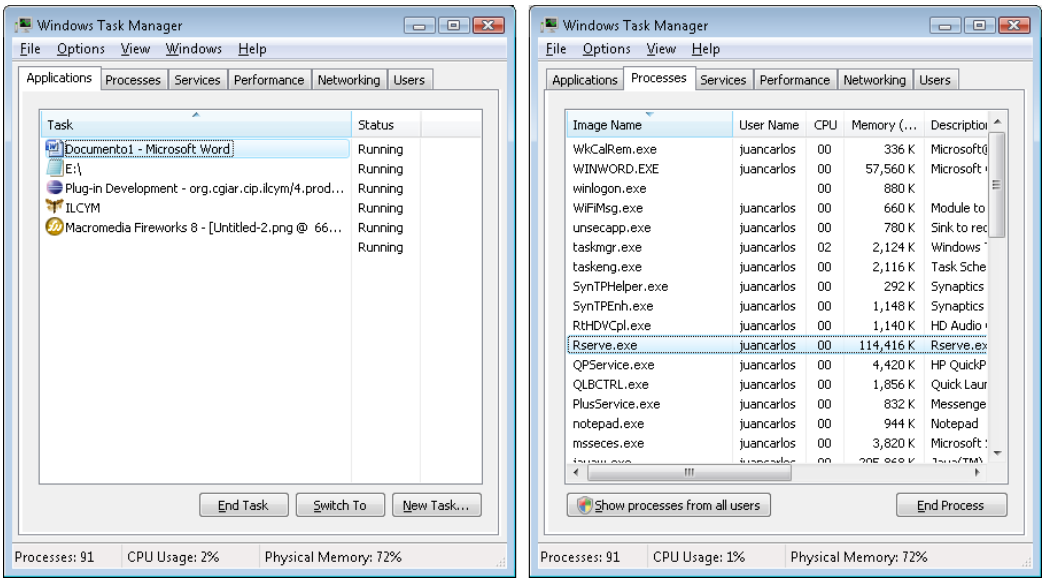
You can select any of the life table parameters and visualize the outputs.

IV. ILCYM's common errors

4.1 ILCYM's crashing or hanging

Due to overload of tasks ILCYM software sometimes crash or hang. In such condition the software will run in stand-by and there is disconnection with Rserve. In order to reverse the situation, it is recommended that you terminate all the processes of including Rserve and lunch the software afresh.

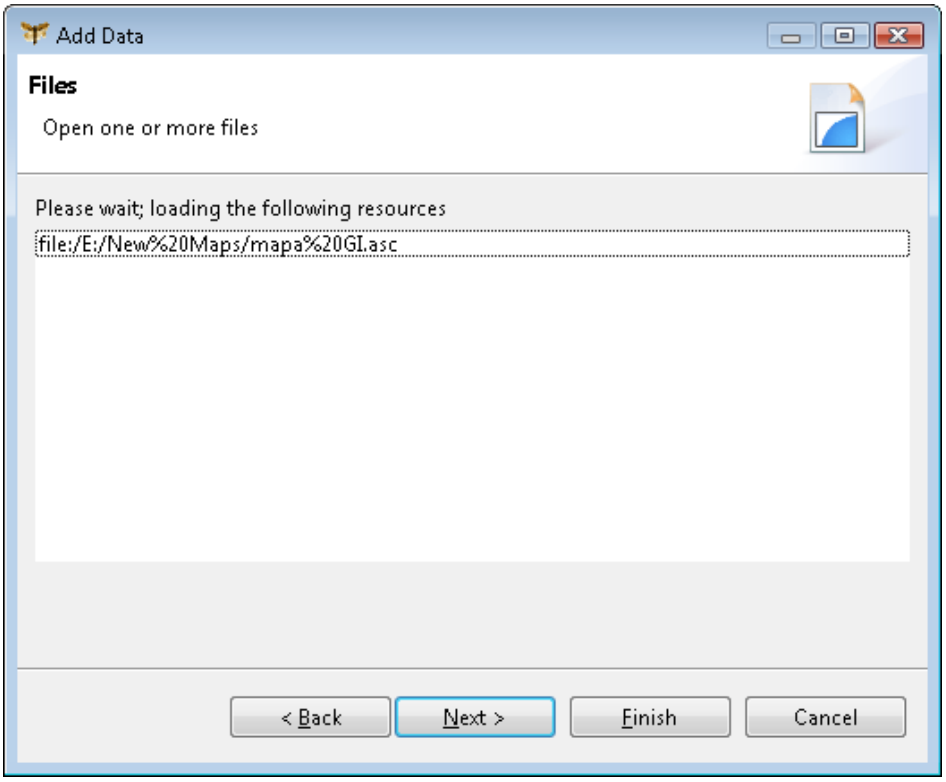
To stop all ILCYM's processes, simultaneously click on Ctrl – Alt – Delete bottoms of your keyboard, then click on task manager, under process, select Rserve.exe and click on EndProcess bottom.

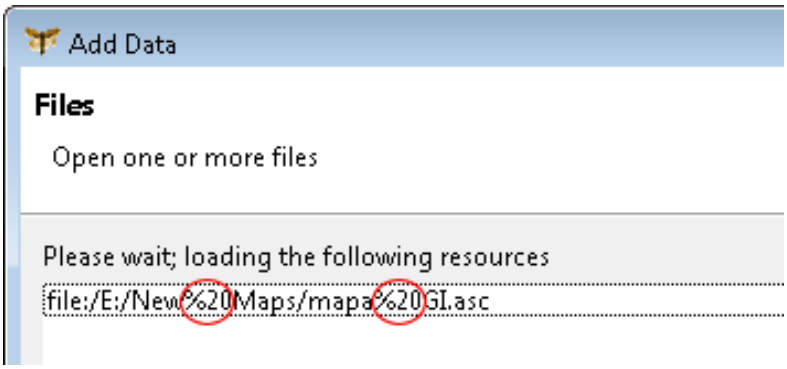

Windows Task Manager
File Options View Windows Help
Applications Processes Services Performance Networking Users
Task Status
Documento1 - Microsoft Word Running
E:\ Running
Plug-in Development - org.cgiar.cip.ilcym/4.prod... Running
ILCYM Running
Macromedia Fireworks 8 - [Untitled-2.png @ 66... Running
Running
End Task Switch To New Task...
Processes: 91 CPU Usage: 2% Physical Memory: 72%
Windows Task Manager
File Options View Help
Applications Processes Services Performance Networking Users
Image Name User Name CPU Memory (... Description
WkCalRem.exe juancarlos 00 336 K Microsoft
WINWORD.EXE juancarlos 00 57,560 K Microsoft
winlogon.exe 00 880 K
WiFiMsg.exe juancarlos 00 660 K Module to
unsecapp.exe juancarlos 00 780 K Sink to rec
taskmgr.exe juancarlos 02 2,124 K Windows
taskeng.exe juancarlos 00 2,116 K Task Sche
SynTPHelper.exe juancarlos 00 292 K Synaptics
SynTPEnh.exe juancarlos 00 1,148 K Synaptics
RtHDVCpl.exe juancarlos 00 1,140 K HD Audio
Rserve.exe juancarlos 00 114,416 K Rserve.ex
QPService.exe juancarlos 00 4,420 K HP QuickP
QLBCTRL.exe juancarlos 00 1,856 K Quick Laur
PlusService.exe juancarlos 00 832 K Messenge
notepad.exe juancarlos 00 944 K Notepad
msseces.exe juancarlos 00 3,820 K Microsoft
Show processes from all users End Process
Processes: 91 CPU Usage: 1% Physical Memory: 72%

4.2 Loading map

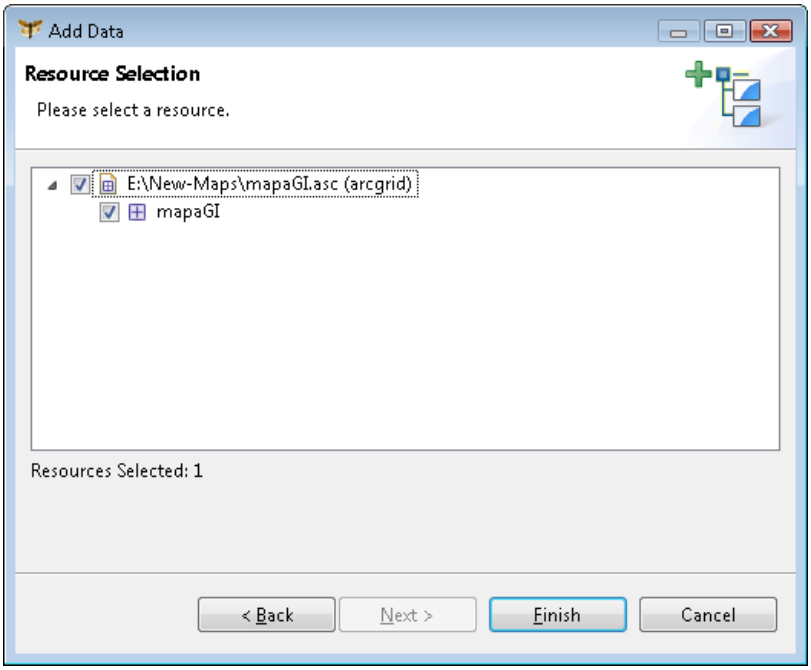
In some cases, an error message may occur when you are loading a map in ILCYM, this happens because the engine of the ILCYM-GIS component (**Udig**)**,** does not allow paths containing spaces blank. For example, the route of the map that you want to upload may look like: "**E: /New Maps/map GI.asc**", in this case you have two blank spaces, the first between New and Maps and the second blank space between map and GI.asc.

In your screen the error will appear on the window as follow

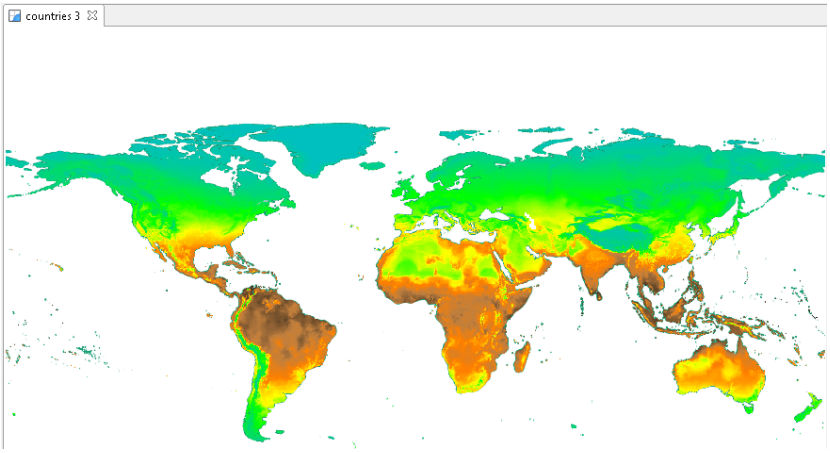




Udig recognizes the blank spaces as " % 20 ", for not having this type of problems, it is best to avoid the blank spaces on the route while naming your map file, to correct the error you need to rewrite the name of the above error as: "**E: /New_Maps/mapa_GI.asc**" or also, "**E:/ New-Maps /map-GI.asc**" or "**E: /NewMaps/**



When you have correct the error, click finish and the map will appear on ILCYM's output window as shown below.



V. Glossary

Activity Index: This index is used in risk mapping and is explicitly related to the finite rate of population increase.

Actual oviposition time: This tern is use to represent the female parasitoid exact length of the oviposition period.

Age Distribution: The proportion of individuals in a population of same age in each class.

Age-Specific Fertility Rate: The number of progenies per individual within a specific age interval during a specified time.

Age-Specific Mortality Rate: The fraction of individuals in a population that die during a given age interval.

Doubling Time: The time it would take a population to double, given no changes in age-specific mortality or fertility rates. Any change in the fertility or the mortality graphs changes doubling time.

Establishment Risk Index: This index is used in risk mapping and identifies those areas in which an insect pest may survive. The index is 1 when a certain proportion of all immature life stages of the pest survive throughout the year.

Finite Rate of Increase (Lambda): A measure of the rate of growth of a population. The amount that the population must be multiplied by to give the population size in the next time unit (assuming the population is in stable age distribution) .

Generation Index: This index is used in risk mapping and estimates the mean number of generations that may be produced within a year.

Generation Time: The average age at which a female gives birth to her offspring. This is equivalent to the time that it takes for a population to increase by a factor equal to the Net Reproductive Rate.

Intrinsic Rate of Increase (rm): A measure of the rate of growth of a population. This is the instantaneous rate of change (per individual per time interval), assuming the population is in stable age distribution. It is equal to the natural log (In) of the Finite Rate of Increase.

Mean Life Expectancy: How long an individual can be expected to live, on average. This is influenced only by the age-specific mortality graph.

Net Reproductive Rate (Ro): The average number of offspring an individual in a population will produce in his/her lifetime. Unlike the Total Fertility Rate, Ro depends on age specific mortality rates.

Sex Ratio: The fraction of the population that is female. Technically, this value is not a "ratio", but this has become a common way of representing the gender distribution of a population. The primary sex ratio is the proportion of births that are female.

Stable Age Distribution: The age distribution which the population will reach if allowed to progress until there is no longer a change in the distribution.

Survivorship: The probability that an individual survives from age zero to a given age.

Total Fertility Rate (TFR): The total number of offspring a female would have, on average, if she were to live to the maximum age (Compare with Net Reproductive Rate).

VI. References

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Appendix

Table 1. Functions fitted to development time in ILCYM software

ID	Function	Expression	Reference
Dichotomy functions			
1	Logit	$F_i(X_1) = P(Y = 1/ X_1, X_{2i}) = \frac{1}{1+e^{-(B_1X_1+B_{2i}X_{2i})}}$	
2	Probit	$E[Y/X] = P(Y=1/X_1, X_{2i}) = \int_{-\infty}^{z} \frac{1}{\sqrt{2\pi}} e^{\left(\frac{-t^2}{2}\right)} dt$ $Z = B_1X_1 + B_{2i}X_{2i}$ $F_i(X_1) = E[Y/X] = \Phi(Z) = \Phi(B_1X_1 + B_{2i}X_{2i})$ $\Phi^{-1}(P(Y=1/X_1, X_{2i})) = B_1X_1 + B_{2i}X_{2i}$	
3	Cloglog	$F_i(X_1) = P(Y=1/X_1, X_2) = 1 - e^{-e^{(B_1X_1+B_{2i}X_{2i})}}$ $\ln(-\ln(P(Y=1))) = B_1X_1 + B_{2i}X_{2i}$	
Exponential functions			
1	Exponential modified 1	$F(X_1) = 1 - e^{-(a*X_1+b*X_1^2+c*X_1^3)}$	
2	Gamma	$f(x) = \frac{1}{b^a * \Gamma(a)} T^{a-1} e^{-\left(\frac{x}{b}\right)}$ $F(X_1) = \int_0^{X_1} (f(x)) \partial x$	
3	Exponential modified 2	$F(X_1) = \frac{1}{1+e^{(a+b*X_1)}}$	
4	Exponential modified 3	$F(X_1) = 1 - e^{-a*X_1^b}$	
5	Exponential modified 4	$F(X_1) = 1 - e^{-\left(\frac{X_1-a}{n}\right)^b}$	
6	Weibull	$F(X_1) = 1 - e^{-\left(\frac{X_1}{b}\right)^a}$	

For dichotomy functions:

$X_1 =$ natural logarithm of the days observed

$X_{2i} =$ *ith* temperature, considered as a categorical variable, so that the value to replace in the linear part of formula is either 0 or 1.

$$Y = \begin{cases} success(1): \text{The state lasted until the individual turn to next state} \\ failure(0): \text{The state does not change or the individual died before adulthood} \end{cases}$$

For exponential functions:

$F_i(X_1)$ = cumulated relative frequency of the days observed for the ith temperature

$X_1 =$ normalized age (days / median survival time) of each temperature

$F(X_1)$ = cumulated relative frequency of the days observed of each temperature

Table 2. Sub-models fitted to development rate in ILCYM software

ID	Name	Equation	Comment	Reference
1	Sharpe & DeMichele 1	$r(T)=\frac{p'.\frac{T}{T_0'}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0'}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_L}{R}\left(\frac{1}{T_L}-\frac{1}{T}\right)\right]}+e^{\left[\frac{\Delta H_H}{R}\left(\frac{1}{T_H}-\frac{1}{T}\right)\right]}}$ $p'=a+b*T_o'$ $T_o'=\frac{\Delta H_L-\Delta H_H}{R*\log\left(-\frac{\Delta H_L}{\Delta H_H}\right)+\left(\frac{\Delta H_L}{T_L}\right)-\left(\frac{\Delta H_H}{T_L}\right)}$	5P	
2	Sharpe & DeMichele 2	$r(T)=\frac{p'.\frac{T}{T_0}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_L}{R}\left(\frac{1}{T_L}-\frac{1}{T}\right)\right]}+e^{\left[\frac{\Delta H_H}{R}\left(\frac{1}{T_H}-\frac{1}{T}\right)\right]}}$ $p'=a+b*T_o$	6P	
3	Sharpe & DeMichele 3	$r(T)=\frac{p.\frac{T}{T_0}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_L}{R}\left(\frac{1}{T_L}-\frac{1}{T}\right)\right]}+e^{\left[\frac{\Delta H_H}{R}\left(\frac{1}{T_H}-\frac{1}{T}\right)\right]}}$	7P	Sharpe and DeMichele 1977
4	Sharpe & DeMichele 4	$r(T)=p.\frac{T}{T_0}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}$	3P	
5	Sharpe & DeMichele 5	$r(T)=\frac{p.\frac{T}{T_0}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_L}{R}\left(\frac{1}{T_L}-\frac{1}{T}\right)\right]}}$	5P	
6	Sharpe & DeMichele 6	$r(T)=\frac{p.\frac{T}{T_0}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_H}{R}\left(\frac{1}{T_H}-\frac{1}{T}\right)\right]}}$	5P	
7	Sharpe & DeMichele 7	$r(T)=p'.\frac{T}{T_0}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}$ $p'=a+b*T_o'$	2P	

8	Sharpe & DeMichele 8	$r(T)=\frac{p'.\frac{T}{T_0}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_L}{R}\left(\frac{1}{T_L}-\frac{1}{T}\right)\right]}}$ $p'=a+b*T_o'$	4P	
9	Sharpe & DeMichele 9	$r(T)=\frac{p'.\frac{T}{T_0}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_H}{R}\left(\frac{1}{T_H}-\frac{1}{T}\right)\right]}}$ $p'=a+b*T_o'$	4P	
10	Sharpe & DeMichele 10	$r(T)=\frac{p.\frac{T}{T_0'}.e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_L}{R}\left(\frac{1}{T_L}-\frac{1}{T}\right)\right]}+e^{\left[\frac{\Delta H_H'}{R}\left(\frac{1}{T_H'}-\frac{1}{T}\right)\right]}}$ $H_H'=1\ \ T_H'=1$	4P	Sporleder *et al.* (2004)
11	Sharpe & DeMichele 11	$r(T)=\frac{p*\frac{T}{T_0'}*e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_L}{R}\left(\frac{1}{T_L}-\frac{1}{T}\right)\right]}+e^{\left[\frac{\Delta H_H}{R}\left(\frac{1}{T_H}-\frac{1}{T}\right)\right]}}$	6P	
12	Sharpe & DeMichele 12	$r(T)=\frac{P'*\frac{T}{T_0}*e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_L}{R}\left(\frac{1}{T_L}-\frac{1}{T}\right)\right]}+e^{\left[\frac{\Delta H_H}{R}\left(\frac{1}{T_H}-\frac{1}{T}\right)\right]}}$ $P'=a+b*T_0$	5P	
13	Sharpe & DeMichele 13	$r(T)=\frac{P*\frac{T}{T_0}*e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_L}{R}\left(\frac{1}{T_L}-\frac{1}{T}\right)\right]}}$	4P	
14	Sharpe & DeMichele 14	$r(T)=\frac{P*\frac{T}{T_0}*e^{\left[\frac{\Delta H_A}{R}\left(\frac{1}{T_0}-\frac{1}{T}\right)\right]}}{1+e^{\left[\frac{\Delta H_H}{R}\left(\frac{1}{T_H}-\frac{1}{T}\right)\right]}}$	4P	

15	Deva 1	$r(T) = b(T - T_{\min})$ T ≥ Tmax $r(T) = 0$ T < Tmax	2P	Dallwits and Higgins 1992
16	Deva 2	$r(T) = b_1\left(10^{-v^2}\right)\left(1 - b_5 + b_5 v^2\right)$ $v = \frac{\left(u + e^{b_4(u)}\right)}{c_2}$ $u = \frac{(T - b_3)}{(b_3 - b_2)} - c_1$ $c_1 = \frac{1}{1 + 0.28b_4 + 0.72\ln(1 + b_4)}$ $c_2 = \frac{1 + b_4}{1 + 1.5b_4 + 0.39{b_4}^2}$	5P	Dallwits and Higgins 1992
17	Logan 1	$r(T) = Y * (e^{p*T} - e^{\left(p*T_{\max} - \frac{(T_{\max} - T)}{v}\right)})$	4P	Longan 1976
18	Logan 2	$r(T) = \alpha\left(\frac{1}{1 + k * e^{-p*T}} - e^{-\frac{(T_{\max} - T)}{v}}\right)$	5P	Longan 1976
19	Briere 1	$r(T) = a * T(T - T_o)\left(\sqrt{T_{\max} - T}\right)$	3P T ≤ Tmax	Briere et al. 1999
20	Briere 2	$r(T) = a * T(T - T_o)(T_{\max} - T)^d$	d Є Z→T Є R d∉ Z→T≤Tmax	Briere et al. 1999
21	Stinner 1	$r(T) = \frac{R_{\max}\left(1 + e^{k_1 + k_2(T_{opc})}\right)}{1 + e^{k_1 + k_2(T)}}$	4P	Stinner et al. 1974
22	Hilber & logan 1	$r(T) = Y\left(\frac{T^2}{T^2 + d^2} - e^{-\frac{(T_{\max} - T)}{v}}\right)$	4P	Hilber and logan 1983
23	Lactin 1	$r(T) = e^{p*T} - e^{-\frac{(p*T_l - (T - T_l))}{dt}} + \lambda$	4P	Lactin et al. 1995
24	Linear	$r(T) = a + b * T$	2P	
25	Exponential simple	$r(T) = b_1 * e^{b_2 * T}$	2P	
26	Tb model	$r(T) = sy * e^{\left(b(T - T_b) - e^{\left(\frac{b(T - T_b)}{DT_b}\right)}\right)}$	4P	
27	Exponential model	$r(T) = sy * e^{b(T - T_b)}$	3P	
28	Exponential	$r(T) = e^{b(T - T_{\min})} - 1$	2P	
29	Ratkowsky 1	$r(T) = b(T - T_b)^2$	2P	Ratkowsky et al. 1982
30	Davidson	$r(T) = \frac{k}{1 + e^{a - bT}}$	2P	Davidson 1942, 1944

31	Pradham	$r(T) = R_m e^{\left[\frac{-1}{2}\left(\frac{T-T_m}{T_\sigma}\right)^2\right]}$	3P	Pradham 1945
32	Angilletta Jr.	$r(T) = a * e^{\left[-\frac{1}{2}\left(\frac{\lvert T-b\rvert}{c}\right)^d\right]}$	4P	Angilletta Jr. 2006
33	Stinner 2	$r(T) = \frac{MaxDevRate * e^{k_1+k_2T_{opt}}}{1+e^{k_1+k_2T}}$	4P	Stinner 1974
34	Hilbert	$r(T) = \Psi\left[\frac{(T-T_b)^2}{((T-T_b)+D^2)}\right] - e^{-(\frac{T_m-(T-T_b)}{\Delta T})}$	5P	Hilbert and Logan 1983
35	Lactin 2	$r(T) = e^{\rho T} - e^{(\rho T_{Max} - \frac{T_{Max}-T}{\Delta})}$	5P	Lactin et al. 1995
36	Anlytis 1	$r(T) = P\delta^n(1-\delta)^m \quad \delta = \frac{T-T_{mim}}{T_{\max}-T_{\min}}$	5P n Є Z→T Є R mЄ Z→T Є R n∉ Z→T≥Tmin m∉Z→T≤Tmx	Analysis 1977
37	Anlytis 2	$r(T) = [P\delta^n(1-\delta)]^m \quad \delta = \frac{T-T_{mim}}{T_{\max}-T_{\min}}$	5P n Є Z→T Є R mЄ Z→T Є R n∉ Z→T≥Tmin m∉Z→T≤Tmx	Analysis 1980
38	Anlytis 3	$r(T) = a(T-T_{\min})^n(T_{\max}-T)^m$	5P n Є Z→T Є R mЄ Z→T Є R n∉ Z→T≥Tmin m∉Z→T≤Tmx	Analysis 1977
39	Allahyari	$r(T) = P\delta^n(1-\delta^m) \quad \delta = \frac{T-T_{mim}}{T_{\max}-T_{\min}}$	5P n Є Z→T Є R mЄ Z→T Є R n∉ Z→T≥Tmin m∉Z→T≥Tmin	Allahyari 2005
40	Briere 3	$r(T) = a(T-T_b)(T_L-T)^{\frac{1}{2}}$	3P	Briere et al. 1999
41	Briere 4	$r(T) = a(T-T_b)(T_L-T)^{\frac{1}{n}}$ T ≤ T_L	3P	Briere et al. 1999

42	Kontodimas 1	$r(T) = a(T - T_{\min})^2 (T_{\max} - T)$	3P	Kontodimas 2004
43	Kontodimas 2	$r(T) = \frac{2}{D_{\min}(e^{K(T-T_{opt})} + e^{-\lambda(T-T_{opt})})}$	4 P	Kontodimas 2004
44	Kontodimas 3	$r(T) = \frac{T * e^{\left(a-\frac{b}{T}\right)}}{1 + e^{\left(c-\frac{d}{T}\right)} + e^{\left(f-\frac{g}{T}\right)}}$	6P	Kontodimas 2004
45	Ratkowsky 2	$r(T) = \left[a\left(T - T_{\min}\right)\left(1 - e^{b(T-T_{\max})}\right)\right]^2$	4P	Ratkowsky et al. 1982
46	Janish 1	$r(T) = \frac{2}{D_{\min}(e^{K(T-T_{opt})} + e^{-K(T-T_{opt})})}$	3P	
47	Janish 2	$r(T) = \frac{2C}{a^{(T-Tm)} + b^{(T_m - T)}}$	3P	
48	Tanigoshi	$r(T) = a_0 + a_1 T + a_2 T^2 + a_3 T^3$	4P	Tanigoshi and Browne 2004
49	Wang-Lan-Ding	$r(T) = k\frac{\left(1 - e^{-a(T-T_{\min})}\right)\left(1 - e^{b(T-T_{\max})}\right)}{1 + e^{-r(T-c)}}$	7P	Wang et al. 1982
50	Stinner 3	$r(T) = \frac{c_1}{1 + e^{(k_1 + k_2 * T)}}$	3P	
51	Stinner 4	$r(T) = \frac{c_1}{1 + e^{(k_1 + k_2 * T)}} + \frac{c_2}{1 + e^{(k_1 + k_2(2 * To - T))}}$	5P	
52	Logan 3	$r(T) = sy * e^{\left(b\left(T - T_{\min}\right) - e^{\left(b * T_{\max} - \frac{(T_{\max} - (T - T_{\min}))}{Dtb}\right)}\right)}$	5P	
53	Logan 4	$r(T) = \alpha\left(\frac{1}{1 + k * e^{-b(T-T_{\min})}} - e^{-\frac{(T_{\max} - (T - T_{\min}))}{Dt}}\right)$	5P	

54	Logan-5	$r(T)=\alpha\left(\frac{1}{1+k*e^{-b(T)}}-e^{-\frac{(T_{\max}-T)}{Dt}}\right)$	6P	
55	Hilber & logan 2	$r(T)=\psi\left(\frac{T^2}{T^2+D}-e^{-\frac{(T_{\max}-T)}{Dt}}\right)$	4P	
56	Hilber & logan 3	$r(T)=\psi\left(\frac{(T-T_{\min})^2}{(T-T_{\min})^2+D}-e^{-\frac{(T_{\max}-(T-T_{\min}))}{Dt}}\right)+\theta$	6P	
57	Taylor	$r(T)=r_m*e^{-\frac{1}{2}\left(-\frac{(T-T_{opt})}{T_{roh}}\right)^2}$	3P	
58	Lactin 3	$r(T)=e^{\rho*T}-e^{(\rho*T_{Max}-\frac{T_{Max}-T}{\Delta})}+\lambda$	4P	
59	Sigmoid or Logistic	$r(T)=\frac{c_1}{1+e^{a+b*T}}$	3P	

- *T* temperature in Degree Celcius

- *r(T)* development rate at temperature *T*

R= 1987 cal degree (-1) mol(-1)

Table 3. Sub-models fitted to mortality in ILCYM software

ID	Model	Equation	Comment	Reference
1	Quadratic	$m(T) = c + b*T + a*T^2$	3P	
2	Linear root	$m(T) = c + b*T + a\left(\sqrt{T}\right)$	3P	
3	Negative Linear root	$m(T) = c + b*T + a\left(\frac{1}{\sqrt{T}}\right)$	3P	
4	Quadratic negative exponent	$m(T) = c + b*T + a\left(\frac{1}{T^2}\right)$	3P	
5	Linear negative exponent	$m(T) = c + b*T + a\left(\frac{1}{T}\right)$	3P	
6	Logarithmic	$m(T) = c + b*T + a*\log(T)$	3P T ≥ 0	
7	Gaussian denominator	$m(T) = \frac{1}{1 + a*e^{-b\left(\frac{T-c}{d}\right)^2}}$	4P	
8	Gaussian	$m(T) = a*e^{-b\left(\frac{T-T_o}{c}\right)^2}$	4P	
9	Simple gaussian	$m(T) = y_0 + a*e^{-\frac{1}{2}\left(\frac{T-T_o}{b}\right)^2}$	4P	
10	Gaussian with log	$m(T) = y_0 + a*e^{-\frac{1}{2}\left(\frac{\log\left(\left\lvert\frac{T}{T_o}\right\rvert\right)}{b}\right)^2}$	4P	
11	Polynomial model 1	$m(T) = b_1 + b_2 T + b_3 T^d$	4P d ∈ Z→T ∈ R d ∉Z→T ≥ 0	
12	Polynomial model 2	$m(T) = e^{\left(b_1 + b_2*T + b_3*T^2\right)}$	3P	

13	Polynomial model 3	$m(T)=1-\left(\frac{b_4}{1+b_5*e^{\left(b_1+b_2*T+b_3*T^2\right)}}\right)$	5P	
14	Polynomial model 4	$m(T)=e^{\left(b_1+b_2*T+b_3\sqrt{T}\right)}$	T ≥ 0	
15	Polynomial model 5	$m(T)=1-\left(\frac{b_4}{1+b_5*e^{\left(b_1+b_2*T+b_3\sqrt{T}\right)}}\right)$	3P T ≥ 0	
16	Polynomial model 6	$m(T)=e^{\left(b_1+b_2*T+b_3\left(\frac{1}{\sqrt{T}}\right)\right)}$	3P T > 0	
17	Polynomial model 7	$m(T)=1-\left(\frac{b_4}{1+b_5*e^{\left(b_1+b_2*T+b_3\left(\frac{1}{\sqrt{T}}\right)\right)}}\right)$	5P T > 0	
18	Polynomial model 8	$m(T)=e^{\left(b_1+b_2*T+b_3\left(\frac{1}{T}\right)\right)}$	3P T ≠ 0	
19	Polynomial model 9	$m(T)=1-\left(\frac{b_4}{1+b_5*e^{\left(b_1+b_2*T+b_3\left(\frac{1}{T}\right)\right)}}\right)$	5P	
20	Polynomial model 10	$m(T)=e^{\left(b_1+b_2*T+b_3*T^d\right)}$	4P d Є Z→TЄR d ∉Z→T ≥ 0	
21	Polynomial model 11	$m(T)=1-\left(\frac{b_4}{1+b_5*e^{\left(b_1+b_2*T+b_3*T^d\right)}}\right)$	6P d Є Z→T Є R d ∉ Z→T ≥ 0	
22	Polynomial model 12	$m(T)=e^{(b_1+b_2*T+b_3*\log(T))}$	3P T ≥ 0	
23	Polynomial model 13	$m(T)=1-\left(\frac{b_4}{1+b_5*e^{b_1+b_2*T+b_3*\log(T)}}\right)$	5P T ≥ 0	

24	Taylor 1	$m(T)=1-rm*e^{\left(-\frac{1}{2}\left(-\frac{(T-T_{opt})}{T_{roh}}\right)^2\right)}$	3P	
25	Taylor 2	$m(T)=1-rm*e^{\left(-\frac{1}{2}\left(-\frac{(\ln(T)-\ln(T_{opt}))}{T_{roh}}\right)^2\right)}$	3PT ≥ 0	
26	Wang 1	$m(T)=1-\frac{1}{e^{\left(\left(1+e^{\left(-\frac{T-T_{opt}}{B}\right)}\right)\left(1+e^{\left(-\frac{T_{opt}-T}{B}\right)}\right)*H\right)}}$	3P	
27	Wang 2	$m(T)=1-\frac{1}{e^{\left(\left(1+e^{\left(-\frac{T-T_l}{B}\right)}\right)\left(1+e^{\left(-\frac{T_h-T}{B}\right)}\right)*H\right)}}$	4P	
28	Wang 3	$m(T)=1-\frac{1}{e^{\left(\left(1+e^{\left(-\frac{T-T_{opt}}{B_l}\right)}\right)\left(1+e^{\left(-\frac{T_{opt}-T}{B_h}\right)}\right)*H\right)}}$	4P	
29	Wang 4	$m(T)=1-\frac{1}{e^{\left(\left(1+e^{\left(-\frac{T-T_l}{B_l}\right)}\right)\left(1+e^{\left(-\frac{T_h-T}{B_h}\right)}\right)*H\right)}}$	5P	
30	Wang 5	$m(T)=1-\frac{H}{e^{\left(\left(1+e^{\left(-\frac{T-Topt}{B}\right)}\right)\left(1+e^{\left(-\frac{T_{opt}-T}{B}\right)}\right)\right)}}$	3P	
31	Wang 6	$m(T)=1-\frac{H}{e^{\left(\left(1+e^{\left(-\frac{T-T_l}{B}\right)}\right)\left(1+e^{\left(-\frac{T_h-T}{B}\right)}\right)*H\right)}}$	4P	
32	Wang 7	$m(T)=1-\frac{H}{e^{\left(\left(1+e^{\left(-\frac{T-T_{opt}}{B_l}\right)}\right)\left(1+e^{\left(-\frac{T_{opt}-T}{B_h}\right)}\right)*H\right)}}$	4P	

33	Wang 8	$m(T)=1-\frac{H}{e^{\left(\left(1+e^{\left(-\frac{T-T_l}{B_l}\right)}\right)\left(1+e^{\left(-\frac{T_h-T}{B_h}\right)}\right)*H\right)}}$	5P	
34	Shape	$m(T)=Bm+\left(\left(1-\left(\frac{1}{\left(1+e^{A}+e^{B}\right)}\right)\right)*(1-Bm)\right)$ $A=\left(\frac{H_l}{1.987}\right)*\left(\left(\frac{1}{T_l}\right)-\left(\frac{1}{(T+273.15)}\right)\right)$ $B=\left(\frac{H_h}{1.987}\right)*\left(\left(\frac{1}{T_h}\right)-\left(\frac{1}{(T+273.15)}\right)\right)$	5P	
35	Marc	$m(T)=\left(1-e^{-e^{\left(a_1+b_1*T\right)}}\right)+\left(1-e^{-e^{\left(a_2+b_2*T\right)}}\right)$	4P	
36	DeMoivre	$m(T)=(w-T)^{-1}$	1P	
37	Gompertz	$m(T)=a_1*e^{(b_1*T)}+a_2*e^{(b_2*T)}$	4P	
38	Gompertz-Makeham	$m(T)=a_1*e^{(b_1*T)}+a_2*e^{(b_2*T)}+c_1$	5P	
39	Weibull	$m(T)=a*(\lvert T-b\rvert)^n$	3P	
40	Briere 1	$m(T)=a*T(T-To)(Tl-T)^{\left(\frac{1}{d}\right)}$	4P T ≤ Tl	
41	Briere 2	$m(T)=e^{\left(a*T(T-To)(Tl-T)^{\frac{1}{d}}\right)}$	4P T ≤ Tl	
42	Analytis	$m(T)=a(T-T_{\min})^n(T_{\max}-T)^m$	5P n Є Z→T Є R mЄ Z→T Є R n∉ Z→T≥Tmin m∉Z→T≤ Tmax	

43	Janisch & Analytis	$m(T)=\frac{1}{\left(\frac{D_{\min}}{2}\right)\left(e^{k(T-T_p)}+e^{-\lambda(T-T_p)}\right)}$	4P	
44	Wang 9	$m(T)=a\left(1-\left(e^{\left(-\frac{T-T_l}{B}\right)}\right)\left(1-\left(e^{\left(-\frac{T_h-T}{B}\right)}\right)\right)\right)$	4P	
45	Wang 10	$m(T)=e^{\left(a\left(1-\left(e^{\left(-\frac{T-T_l}{B}\right)}\right)\left(1-\left(e^{\left(-\frac{T_h-T}{B}\right)}\right)\right)\right)\right)}$	5P	

- *T* temperature in Celcius
- *m(T)* mortality function at temperature

Table 4. Sub-models fitted to adult senescence in ILCYM software

The sub-models fitted to adult senescence in ILCYM software are the same (they also maintain their respective ID) as shown in Table 2 excluding the sub-models listed below:

ID	Name
1	Sharpe & DeMichele 1
2	Sharpe & DeMichele 2
3	Sharpe & DeMichele 3
4	Sharpe & DeMichele 4
5	Sharpe & DeMichele 5
6	Sharpe & DeMichele 6
7	Sharpe & DeMichele 7
8	Sharpe & DeMichele 8
9	Sharpe & DeMichele 9
10	Sharpe & DeMichele 10
15	Deva 1
16	Deva 2
17	Logan 1
18	Logan 2
19	Briere 1
20	Briere 2
21	Stinner
22	Hilber & logan
23	Lactin 1
36	Anlytis 1
37	Anlytis 2

38	Anlytis 3
39	Allahyari
40	Briere 3
41	Briere 4
42	Kontodimas 1
43	Kontodimas 2
45	Ratkowsky 2

Table 5. Sub-models fitted to total oviposition in ILCYM software

The sub-models fitted to adult total oviposition in ILCYM software are the same (they also maintain their respective ID) as shown in Table 3 without the sub-models listed below:

ID	Name
26	Wang 1
27	Wang 2
28	Wang 3
29	Wang 4
35	Marc
36	DeMoivre

Table 6. Functions fitted to relative oviposition in ILCYM software

ID	Function	Expression	Reference
1	Exponential modified 1	$l(T)=1-e^{-\left(a*T+b*T^2+c*T^3\right)}$	
2	Gamma	$f(x)=\frac{1}{b^a*\Gamma(a)}T^{a-1}e^{-\left(\frac{x}{b}\right)}$ $l(T)=\int_0^T\left(f(x)\right)\partial x$	
3	Exponential modified 2	$l(T)=\frac{1}{1+e^{(a+b*T)}}$	
4	Exponential modified 3	$l(T)=1-e^{-a*T^b}$	
5	Exponential modified 4	$l(T)=1-e^{-\left(\frac{T-a}{n}\right)^b}$	
6	Weibull	$l(T)=1-e^{-\left(\frac{T}{b}\right)^a}$	

- *T* temperature in Celcius
- *l(T)* relative oviposition function at temperature

Table 7. Functions fitted to oviposition time in ILCYM software

The functions fitted to parasitoid oviposition time in ILCYM software are the same (they also maintain their respective ID) as in shown Table 6.

Table 8. Sub-models fitted to temperature parasitoid rate in ILCYM software

The sub-models fitted to temperature dependent parasitoid rate in ILCYM software are the same (they also maintain their respective ID) as shown in Table 3.